Input file ftmzb48h10; Output File ftmzb48h10.pat
Sequence length 3637

```
GTCGACCCACGCGTCCGCACTCAACAATGCCTGCCCCTCTCTGACTGCACCGTCCCGCCGCCGCTGCCGCCGCCGCGCC   79

CAAGCCAAGTCGAGCGGGGGCGTTGCCCACCGACGGCACAGCCCTTGGGCCCGCCCGGGACCAGGAGGTGAGCCGCGCG   158

                                                                      M   H   S   P     4
CGCACAGCTCCGTGCGCTCGCCCGTCTGAGCGCCCGCCAGGTGCCCCGCAGCCCGCCGCCGAG ATG CAC AGC CCG   233
```

```
 P   G   L   L   A   L   W   L   C   A   V   L   C   A   S   A   R   G   G   S    24
CCT GGG CTC CTG GCG CTG TGG CTT TGC GCT GTG CTG TGC GCA TCG GCG CGC GGG GGC AGC   293

 D   P   Q   P   G   P   G   R   P   A   C   P   A   P   C   H   C   Q   E   D    44
GAC CCC CAG CCT GGC CCG GGG CGT CCC GCC TGC CCG GCT CCC TGC CAC TGC CAG GAG GAC   353

 G   I   M   L   S   A   D   C   S   E   L   G   L   S   V   V   P   A   D   L    64
GGC ATC ATG CTG TCC GCT GAC TGC TCC GAG CTC GGG CTC TCA GTG GTG CCT GCG GAC CTG   413

 D   P   L   T   A   Y   L   D   L   S   M   N   N   L   T   E   L   Q   P   G    84
GAC CCC CTG ACG GCT TAC CTA GAC CTC AGT ATG AAC AAC CTC ACG GAG CTT CAG CCG GGT   473

 L   F   H   H   L   R   F   L   E   E   L   R   L   S   G   N   H   L   S   H   104
CTC TTC CAC CAC CTG CGC TTC CTG GAG GAG CTG CGG CTC TCA GGG AAC CAC CTC TCA CAC   533

 I   P   G   Q   A   F   S   G   L   H   S   L   K   I   L   M   L   Q   S   N   124
ATC CCG GGA CAG GCA TTC TCC GGC CTC CAC AGC CTC AAA ATT CTA ATG CTG CAG AGC AAC   593

 Q   L   R   G   I   P   A   E   A   L   W   E   L   P   S   L   Q   S   L   R   144
CAG CTC CGT GGG ATC CCA GCA GAG GCA CTA TGG GAG CTG CCC AGC CTG CAG TCG CTG CGC   653

 L   D   A   N   L   I   S   L   V   P   E   R   S   F   E   G   L   S   S   L   164
CTA GAT GCT AAT CTC ATC TCC CTG GTC CCT GAG AGA AGC TTT GAG GGG CTC TCC TCC CTC   713

 R   H   L   W   L   D   D   N   A   L   T   E   I   P   V   R   A   L   N   N   184
CGC CAC CTC TGG CTG GAT GAC AAT GCA CTC ACT GAG ATC CCC GTC AGA GCT CTC AAC AAC   773

 L   P   A   L   Q   A   M   T   L   A   L   N   H   I   R   H   I   P   D   Y   204
CTT CCT GCC CTA CAG GCC ATG ACC TTG GCT CTC AAC CAT ATC CGC CAC ATC CCT GAC TAT   833

 A   F   Q   N   L   T   S   L   V   V   L   H   L   H   N   N   R   I   Q   H   224
GCC TTC CAG AAC CTC ACC AGT CTT GTG GTG CTG CAT CTA CAT AAC AAC CGC ATC CAG CAT   893

 V   G   T   H   S   F   E   G   L   H   N   L   E   T   L   D   L   N   Y   N   244
GTG GGG ACC CAC AGC TTC GAG GGG CTG CAC AAT CTG GAG ACA CTA GAC CTG AAC TAT AAT   953

 E   L   Q   E   F   P   L   A   I   R   T   L   G   R   L   Q   E   L   G   F   264
GAG CTG CAG GAG TTC CCC TTG GCT ATC CGG ACC CTG GGC AGG CTG CAG GAA TTG GGT TTC   1013

 H   N   N   N   I   K   A   I   P   E   K   A   F   M   G   N   P   L   L   Q   284
CAT AAC AAC AAC ATC AAG GCT ATC CCA GAG AAA GCC TTC ATG GGC AAC CCT CTC CTG CAG   1073

 T   I   H   F   Y   D   N   P   I   Q   F   V   G   R   S   A   F   Q   Y   L   304
ACA ATA CAT TTT TAT GAC AAC CCA ATC CAG TTT GTG GGA AGG TCA GCA TTC CAG TAC CTG   1133

 S   K   L   H   T   L   S   L   N   G   A   T   D   I   Q   E   F   P   D   L   324
TCT AAA CTG CAT ACG CTA TCT TTG AAT GGT GCC ACT GAT ATC CAA GAG TTC CCA GAC CTC   1193

 K   G   T   T   S   L   E   I   L   T   L   T   R   A   G   I   R   L   L   P   344
AAA GGC ACC ACT AGC CTG GAG ATC CTG ACC CTG ACC CGT GCG GGC ATC AGA CTG CTC CCA   1253
```

Figure 1

```
  P   G   V   C   Q   Q   L   P   R   L   R   I   L   E   L   S   H   N   Q   I   364
CCG GGA GTG TGC CAA CAG CTG CCT AGG CTC CGA ATC CTG GAG CTG TCT CAT AAT CAG ATC  1313

  E   E   L   P   S   L   H   R   C   Q   K   L   E   E   I   G   L   R   H   N   384
GAG GAG TTA CCC AGC CTG CAC AGA TGT CAG AAG CTG GAG GAA ATT GGC CTC CGA CAT AAC  1373

  R   I   K   E   I   G   A   D   T   F   S   Q   L   G   S   L   Q   A   L   D   404
AGG ATC AAG GAA ATT GGT GCA GAT ACC TTC AGC CAG CTG GGC TCC TTG CAA GCT TTA GAC  1433

  L   S   W   N   A   I   R   A   I   H   P   E   A   F   S   T   L   R   S   L   424
CTG AGT TGG AAT GCC ATC CGT GCC ATC CAC CCT GAG GCT TTC TCA ACC CTT CGA TCC TTG  1493

  V   K   L   D   L   T   D   N   Q   L   T   T   L   P   L   A   G   L   G   G   444
GTT AAG CTG GAC CTG ACT GAC AAC CAG CTG ACC ACA CTG CCC CTG GCT GGG CTG GGA GGC  1553

  L   M   H   L   K   L   K   G   N   L   A   L   S   Q   A   F   S   K   D   S   464
CTG ATG CAC CTG AAG CTC AAA GGG AAC TTG GCC CTG TCT CAG GCC TTC TCC AAG GAC AGT  1613

  F   P   K   L   R   I   L   E   V   P   Y   A   Y   Q   C   C   A   Y   G   I   484
TTC CCA AAA CTG AGG ATC CTG GAG GTG CCC TAC GCC TAC CAG TGC TGT GCC TAC GGC ATC  1673

  C   A   S   F   F   K   T   S   G   Q*  W   Q   A   E   D   F   H   P   E   E   504
TGT GCC AGC TTC TTC AAG ACC TCT GGG CAG TGG CAG GCC GAG GAC TTT CAT CCA GAA GAA  1733

  E   E   A   P   K   R   P   L   G   L   L   A   G   Q   A   E   N   H   Y   D   524
GAG GAG GCA CCA AAG AGG CCC CTG GGT CTC CTT GCT GGA CAA GCT GAG AAC CAC TAT GAC  1793

  L   D   L   D   E   L   Q   M   G   T   E   D   S   K   P   N   P   S   V   Q   544
CTA GAC CTG GAT GAG CTC CAG ATG GGG ACA GAG GAC TCA AAG CCA AAC CCC AGT GTC CAG  1853

  C   S   P   V   P   G   P   F   K   P   C   E   H   L   F   E   S   W   G   I   564
TGC AGC CCT GTT CCA GGC CCC TTC AAG CCC TGC GAG CAC CTC TTT GAG AGC TGG GGC ATC  1913

  R   L   A   V   W   A   I   V   L   L   S   V   L   C   N   G   L   V   L   L   584
CGC CTT GCT GTG TGG GCC ATC GTG CTG CTC TCC GTA CTC TGT AAC GGG CTG GTG CTG CTG  1973

  T   V   F   A   S   G   P   S   P   L   S   P   V   K   L   V   V   G   A   M   604
ACA GTC TTT GCC AGC GGA CCC AGC CCG CTG TCC CCC GTC AAG CTT GTG GTG GGT GCG ATG  2033

  A   G   A   N   A   L   T   G   I   S   C   G   L   L   A   S   V   D   A   L   624
GCA GGC GCC AAC GCC CTG ACG GGC ATT TCC TGT GGT CTC CTG GCC TCT GTG GAC GCC TTG  2093

  T   Y   G   Q   F   A   E   Y   G   A   R   W   E   S   G   L   G   C   Q   A   644
ACC TAT GGT CAG TTC GCT GAG TAT GGA GCC CGC TGG GAG AGC GGT CTG GGC TGC CAG GCT  2153

  T   G   F   L   A   V   L   G   S   E   A   S   V   L   L   L   T   L   A   A   664
ACG GGC TTC CTG GCT GTC CTG GGT TCA GAG GCG TCG GTG CTG CTG CTC ACA CTG GCG GCC  2213

  V   Q   C   S   I   S   V   T   C   V   R   A   Y   G   K   A   P   S   P   G   684
GTG CAG TGC AGC ATC TCT GTG ACC TGC GTC CGA GCC TAC GGG AAG GCG CCG TCG CCT GGC  2273

  S   V   R   A   G   A   L   G   C   L   A   L   A   G   L   A   A   A   L   P   704
AGC GTC CGC GCA GGC GCA CTG GGA TGC CTG GCG CTG GCC GGG CTG GCC GCA GCA CTG CCG  2333

  L   A   S   V   G   E   Y   G   A   S   P   L   C   L   P   Y   A   P   P   E   724
CTG GCC TCG GTG GGA GAG TAT GGC GCC TCC CCA CTC TGC CTG CCC TAC GCC CCA CCC GAG  2393

  G   R   P   A   A   L   G   F   A   V   A   L   V   M   M   N   S   L   C   F   744
GGC CGG CCG GCC GCC CTG GGC TTC GCT GTA GCC CTG GTG ATG ATG AAC TCG CTC TGC TTC  2453
```

Figure 1 (Cont'd)

```
L   V   V   A   G   A   Y   I   K   L   Y   C   D   L   P   R   G   D   F   E   764
CTG GTG GTG GCC GGC GCC TAC ATC AAG CTC TAC TGT GAC CTG CCA CGG GGT GAC TTT GAG   2513

A   V   W   D   C   A   M   V   R   H   V   A   W   L   I   F   A   D   G   L   784
GCC GTG TGG GAC TGC GCC ATG GTG CGC CAC GTG GCC TGG CTC ATC TTT GCA GAT GGC CTC   2573

L   Y   C   P   V   A   F   L   S   F   A   S   M   L   G   L   F   P   V   T   804
CTC TAC TGC CCC GTG GCC TTC CTC AGC TTT GCC TCC ATG CTG GGC CTC TTC CCT GTC ACC   2633

P   E   A   V   K   S   V   L   L   V   V   L   P   L   P   A   C   L   N   P   824
CCC GAG GCT GTC AAG TCA GTC CTT CTG GTG GTG CTG CCT CTG CCT GCC TGC CTC AAC CCA   2693

L   L   Y   L   L   F   N   P   H   F   R   D   D   L   R   R   L   W   P   S   844
CTG CTC TAC CTG CTC TTC AAC CCT CAC TTC CGG GAT GAC CTT CGG CGG CTC TGG CCA AGC   2753

P   R   S   P   G   P   L   A   Y   A   A   A   G   E   L   E   K   S   S   C   864
CCT CGG TCC CCA GGG CCC CTA GCC TAC GCT GCA GCC GGT GAG CTG GAG AAG AGC TCC TGC   2813

D   S   T   Q   A   L   V   A   F   S   D   V   D   L   I   L   E   A   S   E   884
GAC TCC ACC CAA GCG CTG GTG GCT TTC TCA GAT GTG GAT CTT ATT CTG GAA GCT TCT GAG   2873

A   G   Q   P   P   G   L   E   T   Y   G   F   P   S   V   T   L   I   S   R   904
GCT GGG CAG CCT CCT GGG CTA GAG ACC TAT GGC TTC CCT TCA GTG ACC CTC ATC TCC CGA   2933

H   Q   P   G   A   T   R   L   E   G   N   H   F   I   E  -S   D   G   T   K   924
CAT CAG CCG GGG GCC ACC AGG CTG GAG GGA AAC CAT TTT ATA GAG TCT GAT GGA ACC AAG   2993

F   G   N   P   Q   P   P   M   K   G   E   L   L   L   K   A   E   G   A   T   944
TTT GGG AAC CCA CAA CCT CCC ATG AAG GGA GAA CTG CTG CTG AAG GCA GAG GGA GCC ACT   3053

L   A   G   C   G   S   S   V   G   G   A   L   W   P   S   G   S   L   F   A   964
TTG GCA GGC TGT GGC TCT TCC GTG GGT GGA GCC CTC TGG CCC TCT GGC TCT CTC TTT GCC   3113

S   H   L   *                                                                    968
TCT CAC TTG TAA                                                                  3125

ATATCCCTCTCTGTTTGTCCTCTCCCCATCCAATGATGGCTGCTTATAAAAGAAAGACAACTCCAACTCCATAGCAAGA   3204

TGGCCAACACCTCTGACTCCATTGTTCTCTCTCCACGACCCCTAACCAATGAGTGCTTCCAAGTCTTGCTTTGTCTTGG   3283

CCTTCAGCTTCACTTTCACCCTGGGCCTTCTCTGTCCAATCCAATACTTCTGACAGAGGCCTGGGAAATTTGCATAGGA   3362

GAAAGGAGAAAAGCAAAAGACAGTGAAGGTTATTGGGCCCTGACAGAGCCATGATCAGTAAGTGCAGAGTGATGGGGAG   3441

GTCTCACAGAGCATGACACTGGAAGACAACTACCAAAGACATTGGAGAGTCTCCCCTGTGACATATAGAATATAAAATG   3520

TGTTCTGCGTTCCATTAATCTTGACCTATGCTGNGCCAAAGTGCTTCCTGTTAAAATACACTTTGGAAGACATTGAAAA   3599

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC                                     3637
??
```

Figure 1 (Cont'd)

LRR: domain 1 of 8, from 67 to 114: score 46.0, E = 8.1e-10
```
        *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
           +LdLs N+Lt+l pg++++L+ LeeL Ls+N+L+++p ++f++L+
ftmzb048h1
        67  LTAYLDLSMNNLTELQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLH  114
```

LRR: domain 2 of 8, from 115 to 162: score 42.2, E = 1.2e-08
```
         *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
           +L+ L L+ N+L+++p++al+ Lp+L++L L+ N ++ +p+++f++L+
ftmzb048h1
        115  SLKILMLQSNQLRGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS  162
```

LRR: domain 3 of 8, from 163 to 210: score 49.5, E = 7.7e-11
```
         *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
           +L++L+L++N Lt++p al+nLp L+  L N+++++p+++fqnL+
ftmzb048h1
        163  SLRHLWLDDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNLT  210
```

LRR: domain 4 of 8, from 211 to 257: score 39.5, E = 7.4e-08
```
         *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnL k<-*
           +L +L+L nN+++++  +++++L+nLe+LdL++N+L+++p + + L+
ftmzb048h1
        211  SLVVLHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEFPL-AIRTLG  257
```

LRR: domain 5 of 8, from 258 to 305: score 34.1, E = 3.2e-06
```
         *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
           +L+eL + nN+++ +p+ a+ + p L+++++ +N ++ + ++fq L+
ftmzb048h1
        258  RLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLS  305
```

LRR: domain 6 of 8, from 306 to 352: score 23.8, E = 0.0041
```
         *->nLeeLdLsnNk.LtslppgalsnLpnLeeLdLsnNnLtslppglfqn Lk<-*
           +L++L+L++ +++++p+ l++ ++Le L L + ++ lppg++q L+
ftmzb048h1
        306  KLHTLSLNGATdIQEFPD--LKGTTSLEILTLTRAGIRLLPPGVCQQLP  352
```

LRR: domain 7 of 8, from 353 to 398: score 47.6, E = 2.8e-10
```
         *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
           +L+ L+Ls+N++++lp+ l+ +++Lee+ L +N+++++ ++f+ L+
ftmzb048h1
        353  RLRILELSHNQIEELPS--LHRCQKLEEIGLRHNRIKEIGADTFSQLG  398
```

LRR: domain 8 of 8, from 399 to 446: score 49.4, E = 7.9e-11
```
         *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnLk<-*
           +L+ LdLs N ++ ++p+a+s+L++L +LdL +N+Lt+lp + +L
ftmzb048h1
        399 SLQALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLM 446
```

Figure 2

Proteins with leucine-rich repeats

Protein (species)[a]	Function–ligand[a]	Location[a,b]	Repeats[c]	Length[d]	Consensus sequence[d]	PIR[f] entry
					5 10 15 20 25	
RNase inhibitor (porcine)	RNase inhibitor–RNase	Cytoplasm	15	28 (A) 29 (B)	.LE.L.L..C-.LT...C..L..aL.... .L.EL.L..N-.LGD.Ga..L...L..P..	A31857
Leucine-rich α2-GP (human)	?–?	Serum	8	24	.L..L.L..N-.L..-L...LL...--.	NBHUA2
RNA1 (Saccharomyces cerevisiae)	RNA processing–?	Cytoplasm	8	29	.L..L.L..N-.a........a..a......	BVBYN1
U2 snRNP A' (human)	Splicing–U2 snRNP	Nucleus	4	24	.L..L.a..N-.a..-.......L--.	S03616
Biglycan (human)	ECM binding–laminin, fibronectin, TGF-β	ECM	8	24	.L..L.L..N-.I..-a....a...--.	A40757
Decorin (human)	ECM binding–collagen, fibronectin, thrombospondin, TGF-β	ECM	10	24	.L..L.L..N-.I..-V....a..-.--. `	NBHUC8
Fibromodulin (bovine)	ECM binding–collagen, fibronectin	ECM	11	24	.L..L.L..N-.a..-a....a...--.	S05390
Lumican (chicken)	Corneal transparency–?	ECM	12	24	.L..L.L..N-.L..-.....a...--.	A41748
Proteoglycan-Lb (chicken)	?–?	ECM	6	24	.L..a.L..N-.I..-.....a...--.	A41781
Osteoinductive factor (bovine)	Bone morphogenesis–BMP	ECM	6	24	.L..a.L..N-.a......F...--.	A35272
Platelet GP Ibα (human)	Cell adhesion–vWF, thrombin	PM (EC)	7	24	.L..L.L..N-.L..-LP.GL...L--.	NBHUIA
Platelet GP V (human)	Cell adhesion–GP IX, GP Ib	PM (EC)	14	24	.L..L.L..N-.L..-LP..LF..L--.	–
YopM (Yersinia pestis)	Virulence factor–thrombin	IC + EC	12	20	.L..L.a..N-.L..-LP-.----L--PP	A33950
IpaH7.8 (Shigella flexneri)	?–?	?	6	20	.L..L.V..N-.L..-LP-.----L--P.	A35149
IpaH4.5 (Shigella flexneri)	?–?	?	8	20	.L..L.a..N-.L..-LP-.----L--P.	S18248
Toll (Drosophila)	Embryo development–?	PM (EC)	19	24	.L..L.L..N-.L..-......F...--.	A29943
Slit (Drosophila)	Axon development–?	EC	19	24	.L..L.L..N-.I..-......F..L--.	A36665
Connectin (Drosophila)	Synapse development–?	PM (EC)	7 .	24	.L..LNL..N-.I..-a...aF..L--.	S28464
Chaoptin (Drosophila)	Photoreceptor-cell development–?	PM (EC)	30	24	.L..L.L..N-.a..-a....F..a--.	A29944
Flightless-I (Drosophila)	Embryo development–?	PM (EC)	16	23	.L..L.LS.N-.L..-aP..a..-L--.	–
Oligodendrocyte myelin GP (human)	Myelination–?	PM (EC)	8	24	.L..L.LSNN-.a..-a.......L--.	A34210
CD14 (human)	Cell-surface receptor–LPS–LPB	PM (EC)	8	27	.a..L.L..N-................	TDHUM4
Trk (human)	Receptor protein kinase–NGF	PM (EC)	2	23	.L..L.LS.N-.L.....-.-....--.	TVHUTT
TrkB (mouse)	Receptor protein kinase–BDNF, NT-3	PM (EC)	3	23	.L..L.aT.N-.LTS....-.-.....--T	S06943
TrkC (porcine)	Receptor protein kinase–NT-3	PM (EC)	3	23	.LR.aNLSQN-.L...S.-.-....--.	A40026
TMK1 (Arabidopsis thaliana)	Receptor protein kinase–?	PM (EC)	11	23	.L..a.L..N-...G.aP-.-a.SL--.	JQ1674
LH-CG receptor (rat)	Signal transduction–LH, CG	PM (EC)	5	25	.L..L.a..T-.a.......F...--.	A41343
FSH receptor (rat)	Signal transduction–FSH	PM (EC)	7	25	.L..L.aS.T-.....LP...a..a--.	A34548
TSH receptor (dog)	Signal transduction–TSH	PM (EC)	6	25	.a..L.a.NN..a.S-a....a...--.	A40077
Adenylate cyclase (Saccharomyces cerevisiae)	Signal transduction–RAS	PM (cytoplasm)	20	23	.L..L.L..N-.a..-a...-a..L--.	OYBY.
T-LR (Trypanosoma brucei)	?–?	?	18	23	.L..L.LSGC..a..--a..-a..L--.	A36359
RAD1 (Saccharomyces cerevisiae)	DNA repair–RAD10	Nucleus	3	23	.a.LaDI..N--LP..a......N---.	DDBYD1
RAD7 (Saccharomyces cerevisiae)	DNA repair–?	?	5	26	.L..L.a..C..a....a...a...--P	A25226
DRT100 (Arabidopsis thaliana)	Recombination–?	Chloroplast	5	24	.L..LNL..N-.L.G.IP.S-a.S.--.	A46260
GRR1 (Saccharomyces cerevisiae)	Signal transduction–?	Cytoplasm	9	26	.L..a.L..C.NaTD..a..-L..L.-.	A41529
CCR4 (Saccharomyces cerevisiae)	Transcription–?	?	4	23	.L..L.a..N-.LT.-LP.E-a...--.	S31286
sds22 (Schizosaccharomyces pombe)	Mitosis–dis2, sds21	Nucleus	11	22	.L..L.a..N-.I..-a--ENa..L--.	A38439
p34 ribosome-binding protein (rat)	RM membranes–ribosome	RM membrane (cytoplasm)	4	24	.L..LDL..N-.L..-LP...F..L--.	–
Carboxypeptidase N (human)	Stabilization–catalytic subunit	Plasma	12	24	.L..L.L..N-.L..-LP..aF..L--.	A34901
Internalin (Listeria monocytogenes)	Invasion–?	Cell wall	13	22	NL..L.L..N-QISDI.P---L..L--T	A39930
InlB (Listeria monocytogenes)	?–?	?	6	22	.L..L.L..N-.L.DI.----L..L--.	C39930
					5 10 15 20 25	
LRR superfamily					.L..L.L..N±.a..±a±±±±a±±±a±±.±±	

Figure 3

>human DNA seq.

```
TAATACGACTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAA
TTCCCGGGTCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCC
GGCTCATCCAGCCTCTCTTGCTGCCCTAGCGGCCTCCAACACAACCGCATCTG
GGAAATTGGAGCT:GACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATC
TTAGCTGGAACGCCATCCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCAC
TCCCTGGTCAAGCTGGACCTGACAGACAACCAGCTGACCACACTGCCCCTGGC
TGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCC
AGGCCTTCTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATG
CCTACCAGTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGG
CAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCC
CCTGGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGACCTGGATG
AGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCAGTGTCCAGTGTAGC
CCTACTCCAGGCCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCAT
CCGCCTGGCCGTGTGGGCCATCGTGTTGCTCTCCGTGCTCTGCAATGGACTGG
TGCTGCTGACCGTGTTCGCTGGCGGGCCTGCCCCCCTGCCCCCGGTCAAGTTT
GTGGTAGGTGCGATTGCAGGCGCCAACACCTTGACTGGCATTTCCTGTGGCCT
TCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCC
GCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGGCTTCCTGGCAGTACTTGG
GTCGGAGGCATCGGTGCTGCTGCTCACTCTGGCCGCAGTGCAGTGCAGCGTC
TCCGTCTCCTGTGTCCGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGTTCG
AGCAGGGGTCCTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCCGCACTGCCC
CTGGCCTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGC
CACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGAT
GAACTCCTTCTGTTTCCTGGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGA
CCTGCCGCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCAC
GTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCT
CAGCTTCGCCTCCATGCTGGGCCTCTTCCCTGTCACGCCCGAGGCCGTCAAGT
CTGTCCTGCTGGTGGTGCTGCCCCTGCCTGCCTGCCTCAACCCACTGCTGTAC
CTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCCGCGC
AGGGGACTCAGGGCCCCTAGCCTATGCTGCGGCCGGGGGAGCTGGAGAAGAGC
TCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTCTG
GAAGCTTCTGAAGCTGGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTC
AGTGACCCTCATCTCCTGTCAGCAGCCAGGGGCCCCCAGGCTGGAGGGCAGC
CATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCCTCCATGGA
TGGAGAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTG
TCAGGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTCACACGTGTA
AATATCCCTCCCCATTCTTCTCTTCCCCTCTCTTCCCTTTCCTCTCTCCCCCTCG
GTGAATGATGGCTGCTTCTAAAACAAATACAACCAAAACTCAGCAGTGTGATCT
ATAGCAGGATGGCCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGACCAT
CACCAACGGGTGCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCT
TGATACTGGGCCTCTTCCTTGTCATGTCTGAAGCTGTGGACCAGAGACCTGGAC
TTTTGTCTGCTTAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGG
TTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCTGGAAGGT
GATTTCCCGTGTGACTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAAT
CTTGACATATGCCATGCATAAAGACTTCCTATTAAAATAAGCTTTGGAAGAGATT
AAAAAAAAAAAAAAGGGCGGCCGCTCTAGAGGATCCAAGCTTACGTACGCGT
GCATGCGACGTCATAGCTCTTCTATAGTGTCACCTAAATTCAATT
```

Figure 4

>fahr human

NTTHYRESWYACRYRSGIPGSTHASVERSQGLSLPAHPASLAALAASNTTASGKLE
DTFSQLSSLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHL
KLKGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDLHLD
DEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPCEYL
FESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFVVGAIAGANTLTGISCG
LLASVDALTFGQFSEYGARWETGLGCRATGFLAVLGSEASVLLLTLAAVQCSVSVS
CVRAYGKSPSLGSVRAGVLGCLALAGLAAALPLASVGEYGASPLCLPYAPPEGQP
AALGFTVALVMMNSFCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFAD
GLLYCPVAFLSFASMLGLFPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLR
RLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYG
FPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGL
SGGGGFQPSGLAFASHV

Figure 5

```
LRR: domain 1 of 1, from 64 to 111: score 51.0, E = 2.6e-11
            *->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnL
              +L+ LdLs N ++s++p+a+s+L++L +LdL +N+Lt+lp  + +L
     fahr   64   SLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGL 110

            k<-*

     fahr  111 M    111
```

Figure 6

ftmzb048h10
Aa_of_aambb001d112
fahr_human

```
1                                                                       80
MRSPPGLLALMLCAVLCASARGGSDPQPGPGRPACPAPCHCQEDGIMLSADCSELGLSVVPADLDPLTAYLDLSRDNLTE
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
```

ftmzb048h10
Aa_of_aambb001d112
fahr_human

```
81                                                                      160
LQPGLPHHLRPLEELRLSGNHLSHIPGQAFSGLHSLKILMLQSNQLRGIPAEALNELPSLQSLRLDANLISUVPERSPEG
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
```

ftmzb048h10
Aa_of_aambb001d112
fahr_human

```
161                                                                     240
LSSLRHLWLDDNALTEIPVRALNDLPALQAMTLAINHIRHIPDYAFQRLTSLVVLHLHNNRIQHVGTHSFPGLHNLETLD
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
```

ftmzb048h10
Aa_of_aambb001d112
fahr_human

```
241                                                                     320
LAYNELQEFPLAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSAPQYLSKLHTLSINGATDIQE
--------------------------------------------------------------------------------
------------------------NTTHYRES------WYACKYRS------GIPGST------
```

ftmzb048h10
Aa_of_aambb001d112
fahr_human

```
321                                                                     400
PPDLRGTTSLEILALTRAGIRLLPPGVCQQLPRLRILELSHNQIEELPSLHRCQKLEEIGLRFNRIKEIGADTFSQLGSL
------H--ASVE------RSQGLSLP------AHPASLAALAASNTTASG---------KLEX-----------DTFSQLSSL
```

ftmzb048h10
Aa_of_aambb001d112
fahr_human

```
401                                                                     460
QALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLMHLXLXGHLALSQAFSKDSFPKLRILEVPYAYQCC
---------------------------------------MHLXLXGHLALSQAFSKDSFPKLRILEVPYAYQCC
QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLXLXGHLALSQAFSKDSFPKLRILEVPYAYQCC
```

ftmzb048h10
Aa_of_aambb001d112
fahr_human

```
481                                                     560
AYGICASFFKTSGQWQAEDFHPEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSPVPGPFKPCEHLFE
AYGICASFFKTSGQWQAEDFHPEEEEAPKRPLGLLAGQAENHYDLDLDSLQMGTEDSKPHPSVQCSPVPGPFKPCEHLFE
PYGMCASFFKASGQWEAEDLHLDDERSSKRPLGLLARQAENHYDQQLDELQLEMEDSKPHPSVQCSPTPGPFKPCEYLFE
```

ftmzb048h10
Aa_of_aambb001d112
fahr_human

```
561                                                     640
SWGIRLAVWAIVLLSVLCNGLVLLTVFASGPSPLSPVKLVVGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGL
SWGIRLAVWAIVLLSVLCNGLVLLTVFASGPSPLSPVKLVVGAMAGANALSGISCGLLASVDALTYGQFAEYGARWESGL
SWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFVVGAIAGANCLTGISCGLLASVDALTPGQPSEYGARWENGL
```

ftmzb048h10
Aa_of_aambb001d112
fahr_human

```
641           TM I                    TM II                    720
GCQATGFLAVLGSEASVLLLALAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLAAALPLASVGEYGASPLCLPY
GCQATGFLAVLGSEASVLLLALAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLAAALPLASVGEYGASPLCLPY
GCRATGFLAVLGSEASVLLLALAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLAAALPLASVGERYGASPLQLPY
```

TM III   TM IV

ftmzb048h10
Aa_of_aambb001d112
fahr_human

```
721                                                     800
APPEGRPAALGFAVALVMMNSLCFLVVAGAYIRLYCDLPRGQPEAVWDCAMVRHVAMLIFADGLLYCPVAFLSFASMLGL
APPEGRPAALGFAVALVMMNSLCFLVVAGAYIRLYCDLPRGQPEAVWDCAMVRHVAMLIFADGLLYCPVAFLSFASMLGL
APPEGQPAALGFTVALVMMNSFCFLVVAGAYIRLYCDLPRGDFEAVWDCAMVRHVAMLIFADGLLYCPVAFLSFASMLGL
```

TM V   TM VI

ftmzb048h10
Aa_of_aambb001d112
fahr_human

```
801                                                     880
FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNEHFRDDLRRLHPSPRSPGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL
FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNEHFRDDLRRLWPSPRSPGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL
FPVTPEAVKSVLLVVLPLPACLNPLLYLLENEHFRDDLRRLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLIL
```

TM VI

ftmzb048h10
Aa_of_aambb001d112
fahr_human

```
881                                                     960
EASEAGQPPGLETYGFPSVTLISRHQFGATRLEGNHPIESDGTKFGNPQPPMEGELLIKAEGATLAGCGSSVGGALNPSG
EASEAGQPPGLETYGFPSVTLISRHQFGATRLEGNHPVESDGTKFGNPQPPMEGELLIKAEGATLAGCGSSVGGALNPSG
EASEAGRPPGLETYGFPSVTLISCQQFGAPRLEGSHCVEPEGNHFGNPQPSMDGELLIRAEGSTPAGGGLSGGGGFQPSG
```

ftmzb048h10
Aa_of_aambb001d112
fahr_human

```
961          968
SLFASHLN
SLFASHLN
LAFASHVN
```

Figure 7

```
  G   L   H   N   L   E   T   L   D   L   N   Y   N   K   L   Q   E   F   P   V    20
GGG CTG CAC AAT CTG GAG ACA CTA GAC CTG AAT TAT AAC AAG CTG CAG GAG TTC CCT GTG    60

  A   I   R   T   L   G   R   L   Q   E   L   G   F   H   N   N   N   I   K   A    40
GCC ATC CGG ACC CTG GGC AGA CTG CAG GAA CTG GGG TTC CAT AAC AAC AAC ATC AAG GCC   120

  I   P   E   K   A   F   M   G   N   P   L   L   Q   T   I   H   F   Y   D   N    60
ATC CCA GAA AAG GCC TTC ATG GGG AAC CCT CTG CTA CAG ACG ATA CAC TTT TAT GAT AAC   180

  P   I   Q   F   V   G   R   S   A   F   Q   Y   L   P   K   L   H   T   L   S    80
CCA ATC CAG TTT GTG GGA AGA TCG GCA TTC CAG TAC CTG CCT AAA CTC CAC ACA CTA TCT   240

  L   N   G   A   M   D   I   Q   E   F   P   D   L   K   G   T   T   S   L   E   100
CTG AAT GGT GCC ATG GAC ATC CAG GAG TTT CCA GAT CTC AAA GGC ACC ACC AGC CTG GAG   300

  I   L   T   L   T   R   A   G   I   R   L   L   P   S   G   M   C   Q   Q   L   120
ATC CTG ACC CTG ACC CGC GCA GGC ATC CGG CTG CTC CCA TCG GGG ATG TGC CAA CAG CTG   360

  P   R   L   R   V   L   E   L   S   H   N   Q   I   E   E   L   P   S   L   H   140
CCC AGG CTC CGA GTC CTG GAA CTG TCT CAC AAT CAA ATT GAG GAG CTG CCC AGC CTG CAC   420

  R   C   Q   K   L   E   E   I   G   L   Q   H   N   R   I   W   E   I   G   A   160
AGG TGT CAG AAA TTG GAG GAA ATC GGC CTC CAA CAC AAC CGC ATC TGG GAA ATT GGA GCT   480

  D   T   F   S   Q   L   S   S   L   Q   A   L   D   L   S   W   N   A   I   R   180
GAC ACC TTC AGC CAG CTG AGC TCC CTG CAA GCC CTG GAT CTT AGC TGG AAC GCC ATC CGG   540

  S   I   H   P   E   A   F   S   T   L   H   S   L   V   K   L   D   L   T   D   200
TCC ATC CAC CCT GAG GCC TTC TCC ACC CTG CAC TCC CTG GTC AAG CTG GAC CTG ACA GAC   600

  N   Q   L   T   T   L   P   L   A   G   L   G   G   L   M   H   L   K   L   K   220
AAC CAG CTG ACC ACA CTG CCC CTG GCT GGA CTT GGG GGC TTG ATG CAT CTG AAG CTC AAA   660

  G   N   L   A   L   S   Q   A   F   S   K   D   S   F   P   K   L   R   I   L   240
GGG AAC CTT GCT CTC TCC CAG GCC TTC TCC AAG GAC AGT TTC CCA AAA CTG AGG ATC CTG   720

  E   V   P   Y   A   Y   Q   C   C   P   Y   G   M   C   A   S   F   F   K   A   260
GAG GTG CCT TAT GCC TAC CAG TGC TGT CCC TAT GGG ATG TGT GCC AGC TTC TTC AAG GCC   780

  S   G   Q   W   E   A   E   D   L   H   L   D   D   E   E   S   S   K   R   P   280
TCT GGG CAG TGG GAG GCT GAA GAC CTT CAC CTT GAT GAT GAG GAG TCT TCA AAA AGG CCC   840

  L   G   L   L   A   R   Q   A   E   N   H   Y   D   Q   D   L   D   E   L   Q   300
CTG GGC CTC CTT GCC AGA CAA GCA GAG AAC CAC TAT GAC CAG GAC CTG GAT GAG CTC CAG   900

  L   E   M   E   D   S   K   P   H   P   S   V   Q   C   S   P   T   P   G   P   320
CTG GAG ATG GAG GAC TCA AAG CCA CAC CCC AGT GTC CAG TGT AGC CCT ACT CCA GGC CCC   960

  F   K   P   C   E   Y   L   F   E   S   W   G   I   R   L   A   V   W   A   I   340
TTC AAG CCC TGT GAG TAC CTC TTT GAA AGC TGG GGC ATC CGC CTG GCC GTG TGG GCC ATC  1020

  V   L   L   S   V   L   C   N   G   L   V   L   L   T   V   F   A   G   G   P   360
GTG TTG CTC TCC GTG CTC TGC AAT GGA CTG GTG CTG CTG ACC GTG TTC GCT GGC GGG CCT  1080

  A   P   L   P   P   V   K   F   V   V   G   A   I   A   G   A   N   T   L   T   380
GCC CCC CTG CCC CCG GTC AAG TTT GTG GTA GGT GCG ATT GCA GGC GCC AAC ACC TTG ACT  1140
```

FIGURE 8

```
    G    I    S    C    G    L    L    A    S    V    D    A    L    T    F    G    Q    F    S    E    400
   GGC  ATT  TCC  TGT  GGC  CTT  CTA  GCC  TCA  GTC  GAT  GCC  CTG  ACC  TTT  GGT  CAG  TTC  TCT  GAG  1200

    Y    G    A    R    W    E    T    G    L    G    C    R    A    T    G    F    L    A    V    L    420
   TAC  GGA  GCC  CGC  TGG  GAG  ACG  GGG  CTA  GGC  TGC  CGG  GCC  ACT  GGC  TTC  CTG  GCA  GTA  CTT  1260

    G    S    E    A    S    V    L    L    L    T    L    A    A    V    Q    C    S    V    S    V    440
   GGG  TCG  GAG  GCA  TCG  GTG  CTG  CTG  CTC  ACT  CTG  GCC  GCA  GTG  CAG  TGC  AGC  GTC  TCC  GTC  1320

    S    C    V    R    A    Y    G    K    S    P    S    L    G    S    V    R    A    G    V    L    460
   TCC  TGT  GTC  CGG  GCC  TAT  GGG  AAG  TCC  CCC  TCC  CTG  GGC  AGC  GTT  CGA  GCA  GGG  GTC  CTA  1380

    G    C    L    A    L    A    G    L    A    A    A    L    P    L    A    S    V    G    E    Y    480
   GGC  TGC  CTG  GCA  CTG  GCA  GGG  CTG  GCC  GCC  GCA  CTG  CCC  CTG  GCC  TCA  GTG  GGA  GAA  TAC  1440

    G    A    S    P    L    C    L    P    Y    A    P    P    E    G    Q    P    A    A    L    G    500
   GGG  GCC  TCC  CCA  CTC  TGC  CTG  CCC  TAC  GCG  CCA  CCT  GAG  GGT  CAG  CCA  GCA  GCC  CTG  GGC  1500

    F    T    V    A    L    V    M    M    N    S    F    C    F    L    V    V    A    G    A    Y    520
   TTC  ACC  GTG  GCC  CTG  GTG  ATG  ATG  AAC  TCC  TTC  TGT  TTC  CTG  GTC  GTG  GCC  GGT  GCC  TAC  1560

    I    K    L    Y    C    D    L    P    R    G    D    F    E    A    V    W    D    C    A    M    540
   ATC  AAA  CTG  TAC  TGT  GAC  CTG  CCG  CGG  GGC  GAC  TTT  GAG  GCC  GTG  TGG  GAC  TGC  GCC  ATG  1620

    V    R    H    V    A    W    L    I    F    A    D    G    L    L    Y    C    P    V    A    F    560
   GTG  AGG  CAC  GTG  GCC  TGG  CTC  ATC  TTC  GCA  GAC  GGG  CTC  CTC  TAC  TGT  CCC  GTG  GCC  TTC  1680

    L    S    F    A    S    M    L    G    L    F    P    V    T    P    E    A    V    K    S    V    580
   GTC  AGC  TTC  GCC  TCC  ATG  CTG  GGC  CTC  TTC  CCT  GTC  ACG  CCC  GAG  GCC  GTC  AAG  TCT  GTC  1740

    L    L    V    V    L    P    L    P    A    C    L    N    P    L    L    Y    L    L    F    N    600
   CTG  CTG  GTG  GTG  CTG  CCC  CTG  CCT  GCC  TGC  CTC  AAC  CCA  CTG  CTG  TAC  CTG  CTC  TTC  AAC  1800

    P    H    F    R    D    D    L    R    R    L    R    P    R    A    G    D    S    G    P    L    620
   CCC  CAC  TTC  CGG  GAT  GAC  CTT  CGG  CGG  CTT  CGG  CCC  CGC  GCA  GGG  GAC  TCA  GGG  CCC  CTA  1860

    A    Y    A    A    A    G    E    L    E    K    S    S    C    D    S    T    Q    A    L    V    640
   GCC  TAT  GCT  GCG  GCC  GGG  GAG  CTG  GAG  AAG  AGC  TCC  TGT  GAT  TCT  ACC  CAG  GCC  CTG  GTA  1920

    A    F    S    D    V    D    L    I    L    E    A    S    E    A    G    R    P    P    G    L    660
   GCC  TTC  TCT  GAT  GTG  GAT  CTC  ATT  CTG  GAA  GCT  TCT  GAA  GCT  GGG  CGG  CCC  CCT  GGG  CTG  1980

    E    T    Y    G    F    P    S    V    T    L    I    S    C    Q    Q    P    G    A    P    R    680
   GAG  ACC  TAT  GGC  TTC  CCC  TCA  GTG  ACC  CTC  ATC  TCC  TGT  CAG  CAG  CCA  GGG  GCC  CCC  AGG  2040

    L    E    G    S    H    C    V    E    P    E    G    N    H    F    G    N    P    Q    P    S    700
   CTG  GAG  GGC  AGC  CAT  TGT  GTA  GAG  CCA  GAG  GGG  AAC  CAC  TTT  GGG  AAC  CCC  CAA  CCC  TCC  2100

    M    D    G    E    L    L    L    R    A    E    G    S    T    P    A    G    G    G    L    S    720
   ATG  GAT  GGA  GAA  CTG  CTG  CTG  AGG  GCA  GAG  GGA  TCT  ACG  CCA  GCA  GGT  GGA  GGC  TTG  TCA  2160

    G    G    G    G    F    Q    P    S    G    L    A    F    A    S    H    V    *              737
   GGG  GGT  GGC  GGC  TTT  CAG  CCC  TCT  GGC  TTG  GCC  TTT  GCT  TCA  CAC  GTG  TAA            2211

ATATCCCTCCCCATTCTTCTCTTCCCCTCTCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAAACA          2290

AATACAACCAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGA          2369

CCATCACCAACGGGTGCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCTTGATACTGGGCCTCTTCCTTG          2448

TCATGTCTGAAGCTGTGGACCAGAGACCTGGACTTTTGTCTGCTTAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGG          2527
```

FIGURE 8

CONT.

TGGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCTGGAAGGTGATTTCCCGTGTGACTCATG   2606

GATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATATGCCATGCATAAAGACTTCCTATTAAAATAAGCTT   2685

TGGAAGAGATTAAAAAAAAAAAAAAAA   2711
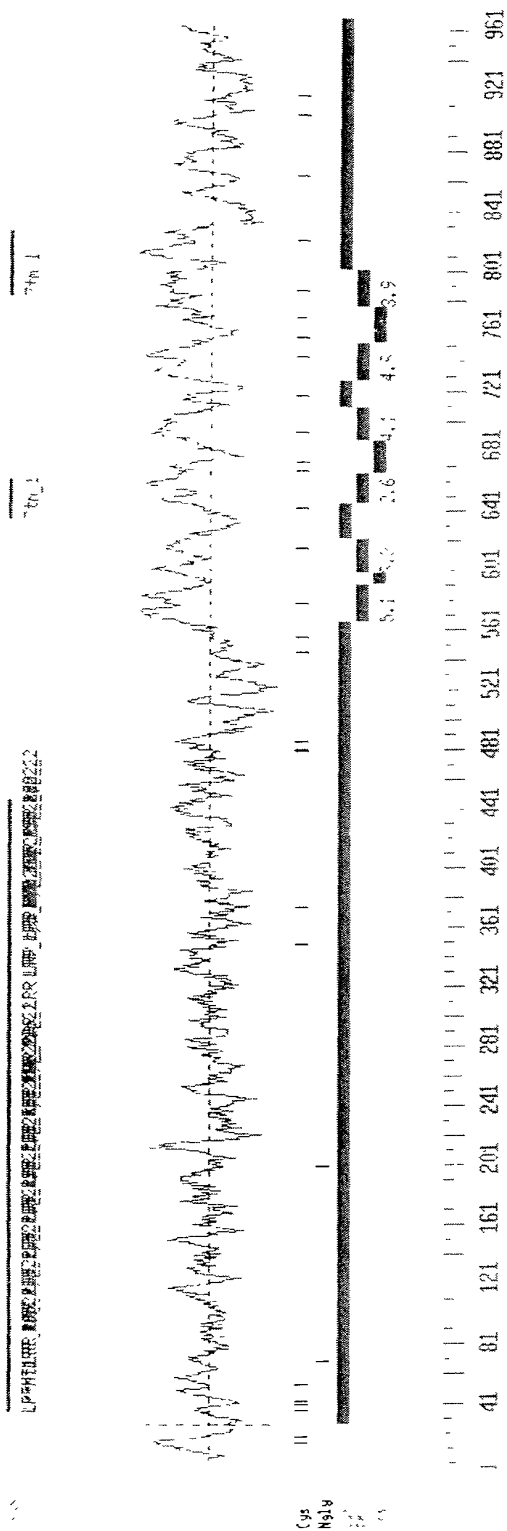
FIGURE 8
CONT.

FIGURE 9

Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1 1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- -
HMM file   /prod/ddm/seqanal/PFAM/pfam6.2/Pfam
Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184 seq
- -

Query: 15088

Scores for sequence family classification (score includes all domains).
Model   Description   Score   E-value N
-------- -----------   -----   ------- ---
LRR   Leucine Rich Repeat   241.4   1 3e-68 16
LRRNT   Leucine rich repeat N-terminal domain   27 2   0.00038 1
7tm_1   7 transmembrane receptor (rhodopsin family) 7 2 0.14   2

Parsed for domains:
Model   Domain seq-f seq-t   hmm-f hmm-t   score E-value
------- ------- ----- -----   ----- -----   ----- -------
LRRNT   1/1   34   65   1   31 []   27 2 0.00038
LRR   1/16   67   90   1   23 []   12 4 11
LRR   2/16   91   114 .   1   23 []   24.2 0.0031
LRR   3/16   115   138 ..   1   23 []   19.9 0.062
LRR   4/16   139   162 .   1   23 []   16 4 0 7
LRR   5/16   163   186 .   1   23 []   27 5 0.00031
LRR   6/16   187   210 ..   1   23 []   12 1 13
LRR   7/16   211   234 .   1   23 []   21.6 0 019
LRR   8/16   235   257   1   23 []   18.2 0.2
LRR   9/16   258   281 .   1   23 []   19 0 0.11
LRR   10/16   282   305 ..   1   23 []   10.2 32
LRR   11/16   306   328 ..   1   23 []   5.6   1.5e+02
LRR   12/16   329   352 .   1   23 []   8.8   52
LRR   13/16   353   374 ..   1   23 []   19.2 0.097
LRR   14/16   375   398 ..   1   23 []   16.9 0.49
LRR   15/16   399   422 ..   1   23 []   23.7 0.0042
LRR   16/16   423   446 ..   1   23 []   16 4 0.66
7tm_1   1/2   635   662 ..   51   79 ..   3.4   2 2
7tm_1   2/2   784   827 .   207 259 .] 1 1   11

Alignments of top-scoring domains:
LRRNT: domain 1 of 1, from 34 to 65: score 27.2, E = 0.00038
              ->aCpreCtCsp..fglvVdCsgrgLtlevPrdlP<-
                aCp++C+C +++ l+ dCs++gL +vP dl
     15088   34   ACPAPCHCQEdgIMLSADCSELGLS-AVPGDLD   65

LRR: domain 1 of 16, from 67 to 90: score 12.4, E = 11
              ->nLeeLdLsnN.LtslppglfsnLp<-
                +LdLs N+Lt+l pglf++L+
     15088   67   LTAYLDLSMNnLTELQPGLFHHLR   90

LRR: domain 2 of 16, from 91 to 114: score 24.2, E = 0.0031
              ->nLeeLdLsnN.LtslppglfsnLp<-
                LeeL+Ls+N+L+++p +fs+L
     15088   91   FLEELRLSGNhLSHIPGQAFSGLY   114

LRR: domain 3 of 16, from 115 to 138: score 19.9, E = 0 062
              ->nLeeLdLsnN LtslppglfsnLp<-
                +L+ L L+nN+L ++p +++ Lp
     15088   115   SLKILMLQNNqLGGIPAEALWELP   138

LRR: domain 4 of 16, from 139 to 162: score 16.4, E = 0 7
              ->nLeeLdLsnN.LtslppglfsnLp<-
                +L++L+L+ N ++ +p+ +f++L+
     15088   139   SLQSLRLDANIISLVPERSFEGLS   162

LRR: domain 5 of 16, from 163 to 186 score 27 5, E = 0 00031
              ->nLeeLdLsnN LtslppglfsnLp<-
                +L++L+L++N Lt++p +++nLp

FIGURE 10

15088   163   SLRHLWLDDNaLTEIPVRALNNLP   186

LRR: domain 6 of 16, from 187 to 210: score 12 1, E = 13
```
              *->nLeeLdLsnN LtslppglfsnLp<-*
                 L+  L N+++++p+ +f+nL+
15088   187   ALQAMTLALNrISHIPDYAFQNLT   210
```


LRR: domain 7 of 16, from 211 to 234: score 21.6, E = 0 019
```
              *->nLeeLdLsnN.LtslppglfsnLp<-*
                +L +L+L+nN++++l ++f++L
15088   211   SLVVLHLHNNrIQHLGTHSFEGLH   234
```


LRR: domain 8 of 16, from 235 to 257. score 18 2, E = 0.2
```
              *->nLeeLdLsnN.LtslppglfsnLp<-*
                 nLe+LdL++N+L+++p +++ L
15088   235   NLETLDLNYNkLQEFPV-AIRTLG   257
```


LRR: domain 9 of 16, from 258 to 281: score 19.0, E = 0.11
```
              *->nLeeLdLsnN.LtslppglfsnLp<-*
                +L+eL ++nN+++ +p+++f + p
15088   258   RLQELGFHNNnIKAIPEKAFMGNP   281
```


LRR: domain 10 of 16, from 282 to 305: score 10 2, E = 32
```
              *->nLeeLdLsnN.LtslppglfsnLp<-*
                 L+++++ +N+++ + ++f+ Lp
15088   282   LLQTIHFYDNpIQFVGRSAFQYLP   305
```


LRR: domain 11 of 16, from 306 to 328: score 5 6, E = 1 5e+02
```
              *->nLeeLdLsnN..LtslppglfsnLp<-*
                +L++L+L++ +++++p+ +++ +
15088   306   KLHTLSLNGAmdIQEFPD--LKGTT   328
```


LRR: domain 12 of 16, from 329 to 352: score 8.8, E = 52
```
              *->nLeeLdLsnN.LtslppglfsnLp<-*
                +Le L L + +++ lp+g +++Lp
15088   329   SLEILTLTRAgIRLLPSGMCQQLP   352
```


LRR: domain 13 of 16, from 353 to 374: score 19.2, E = 0.097
```
              *->nLeeLdLsnN.LtslppglfsnLp<-*
                +L++L Ls+N++++lp+ ++ ++
15088   353   RLRVLELSHNqIEELPS--LHRCQ   374
```


LRR: domain 14 of 16, from 375 to 398: score 16.9, E = 0.49
```
              *->nLeeLdLsnN.LtslppglfsnLp<-*
                +Lee+ L++N++ ++ ++fs+L+
15088   375   KLEEIGLQHNrIWEIGADTFSQLS   398
```


LRR: domain 15 of 16, from 399 to 422: score 23.7, E = 0.0042
```
              *->nLeeLdLsnN.LtslppglfsnLp<-*
                +L+ LdLs N ++s++p++fs L
15088   399   SLQALDLSWNaIRSIHPEAFSTLH   422
```


LRR: domain 16 of 16, from 423 to 446: score 16.4, E = 0.66
```
              *->nLeeLdLsnN.LtslppglfsnLp<-*
                +L +LdL +N+Lt+lp + +L
15088   423   SLVKLDLTDNqLTTLPLAGLGGLM   446
```


7tm_1: domain 1 of 2, from 635 to 662: score 3.4, E = 2.2
```
              *->dWpfGsalCklvtaldvvnmyaSillLta<-*
                +W  G ++C+ +++l v+ + aS+llLt+
15088   635   RWETG-LGCRATGFLAVLGSEASVLLLTL   662
```


7tm_1: domain 2 of 2, from 784 to 827: score 1 1. E = 11
```
              *->lCWlPyfivllJdtlc.lsiimsstCelervlptallvtlwLayvNs
                l+ P +++ +l ++      ++++++v l++ + +
15088   784   LLYCPVAFLSFASMLGlFPV---------TPEAVKSVLLVVLPLPA 820


              clNPilY<-*
              clNP++Y
15088   821 CLNPLLY   827
```


FIGURE 10 cont.

```
//
Searching for complete domains in SMART
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
HMM file:                  /ddm/robison/smart/smart/smart.all.hmms
Sequence file:             /prod/ddm/wspace/orfanal/oa-script.12184.seq
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
 Query:  15088

Scores for sequence family classification (score includes all domains):
Model       Description                                    Score    E-value  N
--------    -----------                                    -----    -------  ---
LRR_typ_2                                                  247.2    2.3e-70  14
LRR_PS_2                                                    78.1    1.8e-19  13
LRR_sd22_2                                                  33.5    4.9e-06   5
lrrnt1                                                      25.7     0.0011   1
LRR_bac_2                                                   11.8          3   7
LRR_RI_2                                                     5.4        7.7   4


Parsed for domains:
Model       Domain  seq-f seq-t    hmm-f hmm-t     score  E-value
--------    ------- ----- -----    ----- -----     -----  -------
lrrnt1       1/1       34    70 ..      1    38 []   25.7   0.0011
LRR_PS_2     1/13      64    87 ..      1    24 []    1.9   1.2e+02
LRR_typ_2    1/14      64    88 ..      1    24 []   12.6      2.1
LRR_bac_2    1/7       89   108 ..      1    20 []    0.9       80
LRR_PS_2     2/13      89   111 ..      1    24 []   17.2      0.4
LRR_typ_2    2/14      89   112 ..      1    24 []   32.1   1.3e-05
LRR_RI_2     1/4       89   115 ..      1    28 []    3.6       14
LRR_bac_2    2/7      113   132 ..      1    20 []    1.6       66
LRR_PS_2     3/13     113   136 ..      1    24 []    1.1   1.5e+02
LRR_typ_2    3/14     113   136 ..      1    24 []   19.2      0.1
LRR_bac_2    3/7      137   156 ..      1    20 []    0.1     1e+02
LRR_PS_2     4/13     137   159 ..      1    24 []    7.1       24
LRR_typ_2    4/14     137   160 ..      1    24 []   25.9  0.00095
LRR_PS_2     5/13     161   183 ..      1    24 []   11.4      6.6
LRR_typ_2    5/14     161   184 ..      1    24 []   27.5  0.00031
LRR_sd22_2   1/5      161   187 ..      1    22 []    5.3       31
LRR_RI_2     2/4      161   190 ..      1    28 []    5.3        8
LRR_PS_2     6/13     185   207 ..      1    24 []    7.0       25
LRR_typ_2    6/14     185   208 ..      1    24 []   23.2   0.0062
LRR_PS_2     7/13     209   232 ..      1    24 []    3.1       79
LRR_typ_2    7/14     209   232 ..      1    24 []   28.1   0.0002
LRR_RI_2     3/4      209   235 ..      1    28 []    1.2       31
LRR_sd22_2   2/5      209   235 ..      1    22 []   13.5        3
LRR_bac_2    4/7      233   252 ..      1    20 []   10.7      4.1
LRR_typ_2    8/14     233   255 ..      1    24 []   16.1     0.76
LRR_PS_2     8/13     233   255 ..      1    24 []   17.1     0.43
LRR_bac_2    5/7      256   275 ..      1    20 []    0.2     1e+02
LRR_PS_2     9/13     256   278 ..      1    24 []    2.9       85
LRR_typ_2    9/14     256   279 ..      1    24 []   24.4   0.0026
LRR_typ_2   10/14     327   350 ..      1    24 []    3.1       29
LRR_bac_2    6/7      351   370 ..      1    20 []   14.6      1.3
LRR_PS_2    10/13     351   372 ..      1    24 []   10.8        8
LRR_sd22_2   3/5      351   372 ..      1    22 []    7.6       16
LRR_typ_2   11/14     351   373 ..      1    24 []   18.8     0.13
LRR_RI_2     4/4      351   378 ..      1    28 []    2.6       19
LRR_PS_2    11/13     373   396 ..      1    24 []    2.3     1e+02
LRR_typ_2   12/14     374   396 ..      1    24 []    6.8       10
LRR_sd22_2   4/5      397   418 ..      1    22 []    7.0       19
LRR_PS_2    12/13     397   419 ..      1    24 []   13.6      3.4
LRR_typ_2   13/14     397   420 ..      1    24 []   30.4   4.3e-05
LRR_bac_2    7/7      421   440 ..      1    20 []    5.8       18
LRR_sd22_2   5/5      421   441 ..      1    22 []    3.7       49
LRR_PS_2    13/13     421   442 ..      1    24 []    5.5       39
LRR_typ_2   14/14     421   444 ..      1    24 []   21.6    0.018

Alignments of top-scoring domains:
```

FIGURE 11

```
lrrnt1: domain 1 of 1, from 34 to 70: score 25.7, E = 0.0011
                  *->qCPapCtCsp.dfgtaVdCsgrgLttlevPldlPadttl<-*
                     +CPapC+C ++    ++ dCs++gL   +vP dl + t +
      15088    34   ACPAPCHCQEdGIMLSADCSELGLS--AVPGDLDPLTAY     70


LRR_PS_2: domain 1 of 13, from 64 to 87: score 1.9, E = 1.2e+02
                  *->LtsL.qvLdLsnNnLsGeIPsslgn<-*
                     L  L+ +LdLs NnL+ e+ + l+
      15088    64   LDPLtAYLDLSMNNLT-ELQPGLFH     87


LRR_typ_2: domain 1 of 14, from 64 to 88: score 12.6, E = 2.1
                  *->LpnL.reLdLsnNqLtsLPpgaFqg<-*
                     L  L+  LdLs N+Lt+L pg+F++
      15088    64   LDPLtAYLDLSMNNLTELQPGLFHH     88


LRR_bac_2: domain 1 of 7, from 89 to 108: score 0.9, E = 80
                  *->PpsLkeLnvsnNrLteLPeL<-*
                      +L+eL+ s+N+L+  P
      15088    89   LRFLEELRLSGNHLSHIPGQ     108


LRR_PS_2: domain 2 of 13, from 89 to 111: score 17.2, E = 0.4
                  *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                     L+ L++L+Ls+N+Ls +IP + ++
      15088    89   LRFLEELRLSGNHLS-HIPGQAFS     111


LRR_typ_2: domain 2 of 14, from 89 to 112: score 32.1, E = 1.3e-05
                  *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                     L+ L+eL+Ls+N+L+++P +aF+g
      15088    89   LRFLEELRLSGNHLSHIPGQAFSG     112


LRR_RI_2: domain 1 of 4, from 89 to 115: score 3.6, E = 14
                  *->npsLreLdLsnNkl.gdeGaraLaeaLks<-*
                     ++ L+eL+Ls+N+l+++ G  +  ++L s
      15088    89   LRFLEELRLSGNHLsHIPG--QAFSGLYS     115


LRR_bac_2: domain 2 of 7, from 113 to 132: score 1.6, E = 66
                  *->PpsLkeLnvsnNrLteLPeL<-*
                      sLk+L  +nN+L   P+
      15088   113   LYSLKILMLQNNQLGGIPAE     132


LRR_PS_2: domain 3 of 13, from 113 to 136: score 1.1, E = 1.5e+02
                  *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                     L sL++L L+nN+L G   + l+
      15088   113   LYSLKILMLQNNQLGGIPAEALWE     136


LRR_typ_2: domain 3 of 14, from 113 to 136: score 19.2, E = 0.1
                  *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                     L +L+ L L+nNqL +P++a++
      15088   113   LYSLKILMLQNNQLGGIPAEALWE     136


LRR_bac_2: domain 3 of 7, from 137 to 156: score 0.1, E = 1e+02
                  *->PpsLkeLnvsnNrLteLPeL<-*
                      psL++L+ + N ++  Pe
      15088   137   LPSLQSLRLDANLISLVPER     156


LRR_PS_2: domain 4 of 13, from 137 to 159: score 7.1, E = 24
                  *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                     L+sLq+L+L  N +s  +P+   +
      15088   137   LPSLQSLRLDANLIS-LVPERSFE     159


LRR_typ_2: domain 4 of 14, from 137 to 160: score 25.9, E = 0.00095
                  *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                     Lp+L++L+L+ N ++ +P++ F+g
      15088   137   LPSLQSLRLDANLISLVPERSFEG     160


LRR_PS_2: domain 5 of 13, from 161 to 183: score 11.4, E = 6.6
                  *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                     L+sL++L L +N L+ eIP     n
      15088   161   LSSLRHLWLDDNALT-EIPVRALN     183


LRR_typ_2: domain 5 of 14, from 161 to 184: score 27.5, E = 0.00031
```

FIGURE 11 cont.

```
lrrnt1: domain 1 of 1, from 34 to 70: score 25.7, E = 0.0011
                  *->qCPapCtCsp.dfgtaVdCsgrgLttlevPldlPadttl<-*
                    +CPapC+C ++     ++ dCs++gL   +vP dl + t +
          15088    34    ACPAPCHCQEdGIMLSADCSELGLS--AVPGDLDPLTAY      70


LRR_PS_2: domain 1 of 13, from 64 to 87: score 1.9, E = 1.2e+02
                  *->LtsL.qvLdLsnNnLsGeIPsslgn<-*
                    L  L+ +LdLs NnL+ e+ + l+
          15088    64    LDPLtAYLDLSMNNLT-ELQPGLFH      87


LRR_typ_2: domain 1 of 14, from 64 to 88: score 12.6, E = 2.1
                  *->LpnL.reLdLsnNqLtsLPpgaFqg<-*
                    L  L+  LdLs N+Lt+L pg+F++
          15088    64    LDPLtAYLDLSMNNLTELQPGLFHH      88


LRR_bac_2: domain 1 of 7, from 89 to 108: score 0.9, E = 80
                  *->PpsLkeLnvsnNrLteLPeL<-*
                     +L+eL+ s+N+L+  P
          15088    89    LRFLEELRLSGNHLSHIPGQ      108


LRR_PS_2: domain 2 of 13, from 89 to 111: score 17.2, E = 0.4
                  *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                    L+ L++L+Ls+N+Ls +IP + ++
          15088    89    LRFLEELRLSGNHLS-HIPGQAFS      111


LRR_typ_2: domain 2 of 14, from 89 to 112: score 32.1, E = 1.3e-05
                  *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                    L+ L+eL+Ls+N+L+++P +aF+g
          15088    89    LRFLEELRLSGNHLSHIPGQAFSG      112


LRR_RI_2: domain 1 of 4, from 89 to 115: score 3.6, E = 14
                  *->npsLreLdLsnNkl.qdeGaraLaeaLks<-*
                    ++ L+eL+Ls+N+l+++ G  +  ++L s
          15088    89    LRFLEELRLSGNHLsHIPG--QAFSGLYS      115


LRR_bac_2: domain 2 of 7, from 113 to 132: score 1.6, E = 66
                  *->PpsLkeLnvsnNrLteLPeL<-*
                     sLk+L  +nN+L   P+
          15088    113    LYSLKILMLQNNQLGGIPAE      132


LRR_PS_2: domain 3 of 13, from 113 to 136: score 1.1, E = 1.5e+02
                  *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                    L sL++L L+nN+L G   + l+
          15088    113    LYSLKILMLQNNQLGGIPAEALWE      136


LRR_typ_2: domain 3 of 14, from 113 to 136: score 19.2, E = 0.1
                  *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                    L +L+ L L+nNqL  +P++a++
          15088    113    LYSLKILMLQNNQLGGIPAEALWE      136


LRR_bac_2: domain 3 of 7, from 137 to 156: score 0.1, E = 1e+02
                  *->PpsLkeLnvsnNrLteLPeL<-*
                     psL++L+ + N ++  Pe
          15088    137    LPSLQSLRLDANLISLVPER      156


LRR_PS_2: domain 4 of 13, from 137 to 159: score 7.1, E = 24
                  *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                    L+sLq+L+L  N +s  +P+  +
          15088    137    LPSLQSLRLDANLIS-LVPERSFE      159


LRR_typ_2: domain 4 of 14, from 137 to 160: score 25.9, E = 0.00095
                  *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                    Lp+L++L+L+ N ++ +P++ F+g
          15088    137    LPSLQSLRLDANLISLVPERSFEG      160


LRR_PS_2: domain 5 of 13, from 161 to 183: score 11.4, E = 6.6
                  *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                    L+sL++L L +N L+ eIP     n
          15088    161    LSSLRHLWLDDNALT-EIPVRALN      183


LRR_typ_2: domain 5 of 14, from 161 to 184: score 27.5, E = 0.00031
```

FIGURE 11 cont.

```
                        *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                          L++Lr+L L++N+Lt++P +a+++
         15088    161    LSSLRHLWLDDNALTEIPVRALNN    184


LRR_sd22_2: domain 1 of 5, from 161 to 187: score 5.3, E = 31
                        *->LtnLeeLdLsqNkI.....kkiENLde<-*
                          L+ L++L+L +N +++ + + + NL
         15088    161    LSSLRHLWLDDNALteipvRALNNLPA    187


LRR_RI_2: domain 2 of 4, from 161 to 190: score 5.3, E = 8
                        *->npsLreLdLsnNklgdeGaraL..aeaLks<-*
                          ++sLr L+L +N l++  +raL++  aL++
         15088    161    LSSLRHLWLDDNALTEIPVRALnnLPALQA    190


LRR_PS_2: domain 6 of 13, from 185 to 207: score 7.0, E = 25
                        *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                          L+ Lq   L+ N++s +IP+  ++
         15088    185    LPALQAMTLALNRIS-HIPDYAFQ    207


LRR_typ_2: domain 6 of 14, from 185 to 208: score 23.2, E = 0.0062
                        *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                          Lp+L+   L N++++P+ aFq+
         15088    185    LPALQAMTLALNRISHIPDYAFQN    208


LRR_PS_2: domain 7 of 13, from 209 to 232: score 3.1, E = 79
                        *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                          LtsL+vL+L+nN++        s+
         15088    209    LTSLVVLHLHNNRIQHLGTHSFEG    232


LRR_typ_2: domain 7 of 14, from 209 to 232: score 28.1, E = 0.0002
                        *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                          L++L +L+L+nN++++L    F+g
         15088    209    LTSLVVLHLHNNRIQHLGTHSFEG    232


LRR_RI_2: domain 3 of 4, from 209 to 235: score 1.2, E = 31
                        *->npsLreLdLsnNklgdeGaraLaeaLks<-*
                          ++sL +L+L nN +   G  + e+L+
         15088    209    LTSLVVLHLHNNRIQHLGTHSF-EGLHN    235


LRR_sd22_2: domain 2 of 5, from 209 to 235: score 13.5, E = 3
                        *->LtnLeeLdLsqNkI.....kkiENLde<-*
                          Lt L++L L +N+I++ +++++E+L++
         15088    209    LTSLVVLHLHNNRIqhlgtHSFEGLHN    235


LRR_bac_2: domain 4 of 7, from 233 to 252: score 10.7, E = 4.1
                        *->PpsLkeLnvsnNrLteLPeL<-*
                          ++L++L+ ++N+L e+P
         15088    233    LHNLETLDLNYNKLQEFPVA    252


LRR_typ_2: domain 8 of 14, from 233 to 255: score 16.1, E = 0.76
                        *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                          L+nL++LdL++N+L++ P  + +
         15088    233    LHNLETLDLNYNKLQEFPVAI-RT    255


LRR_PS_2: domain 8 of 13, from 233 to 255: score 17.1, E = 0.43
                        *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                          L++L++LdL++N+L  e+P  +
         15088    233    LHNLETLDLNYNKLQ-EFPVAIRT    255


LRR_bac_2: domain 5 of 7, from 256 to 275: score 0.2, E = 1e+02
                        *->PpsLkeLnvsnNrLteLPeL<-*
                          +L+eL+  nN+++  Pe
         15088    256    LGRLQELGFHNNNIKAIPEK    275


LRR_PS_2: domain 9 of 13, from 256 to 278: score 2.9, E = 85
                        *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                          L +Lq+L ++nNn+   IP+  +
         15088    256    LGRLQELGFHNNNIK-AIPEKAFM    278


LRR_typ_2: domain 9 of 14, from 256 to 279: score 24.4, E = 0.0026
                        *->LpnLreLdLsnNqLtsLPpgaFqg<-*
```

FIGURE 11 cont.

```
                        L+ L+eL   +nN+++++P+ aF g
           15088    256    LGRLQELGFHNNNIKAIPEKAFMG    279


LRR_typ_2: domain 10 of 14, from 327 to 350: score 3.1, E = 29
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      ++L+ L L +  ++ LP+g++q
           15088    327    TTSLEILTLTRAGIRLLPSGMCQQ    350


LRR_bac_2: domain 6 of 7, from 351 to 370: score 14.6, E = 1.3
                   *->PpsLkeLnvsnNrLteLPeL<-*
                      p+L+ L  s+N+++eLP L
           15088    351    LPRLRVLELSHNQIEELPSL    370


LRR_PS_2: domain 10 of 13, from 351 to 372: score 10.8, E = 8
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L++L+vL+Ls+N++  e+Ps l +
           15088    351    LPRLRVLELSHNQIE-ELPS-LHR    372


LRR_sd22_2: domain 3 of 5, from 351 to 372: score 7.6, E = 16
                   *->LtnLeeLdLsqNkIkkiENLde<-*
                      L +L++L+Ls+N+I+ +   L+
           15088    351    LPRLRVLELSHNQIEELPSLHR    372


LRR_typ_2: domain 11 of 14, from 351 to 373: score 18.8, E = 0.13
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      Lp Lr+L Ls+Nq++LP + ++.
           15088    351    LPRLRVLELSHNQIEELP-SLHRC    373


LRR_RI_2: domain 4 of 4, from 351 to 378: score 2.6, E = 19
                   *->npsLreLdLsnNklgdeGaraLaeaLks<-*
                      +p+Lr+L Ls+N + +    + ++ L++
           15088    351    LPRLRVLELSHNQIEELPSLHRCQKLEE    378


LRR_PS_2: domain 11 of 13, from 373 to 396: score 2.3, E = 1e+02
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      +++L+++ L++N++     +++++
           15088    373    CQKLEEIGLQHNRIWEIGADTFSQ    396


LRR_typ_2: domain 12 of 14, from 374 to 396: score 6.8, E = 10
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      +L+e  L++N++ ++ +++F+
           15088    374    -QKLEEIGLQHNRIWEIGADTFSQ    396


LRR_sd22_2: domain 4 of 5, from 397 to 418: score 7.0, E = 19
                   *->LtnLeeLdLsqNkIkkiENLde<-*
                      L+ L+ LdLs+N I++i
           15088    397    LSSLQALDLSWNAIRSIHPEAF    418


LRR_PS_2: domain 12 of 13, from 397 to 419: score 13.6, E = 3.4
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L+sLq LdLs+N +  +I ++ ++
           15088    397    LSSLQALDLSWNAIR-SIHPEAFS    419


LRR_typ_2: domain 13 of 14, from 397 to 420: score 30.4, E = 4.3e-05
                   *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                      L++L+ LdLs+N+++s++p+aF+
           15088    397    LSSLQALDLSWNAIRSIHPEAFST    420


LRR_bac_2: domain 7 of 7, from 421 to 440: score 5.8, E = 18
                   *->PpsLkeLnvsnNrLteLPeL<-*
                      +sL +L+  +N+Lt+LP
           15088    421    LHSLVKLDLTDNQLTTLPLA    440


LRR_sd22_2: domain 5 of 5, from 421 to 441: score 3.7, E = 49
                   *->LtnLeeLdLsqNkIkkiENLde<-*
                      L+ L+ LdL +N+++ +  L +
           15088    421    LHSLVKLDLTDNQLTTL-PLAG    441


LRR_PS_2: domain 13 of 13, from 421 to 442: score 5.5, E = 39
                   *->LtsLqvLdLsnNnLsGeIPsslgn<-*
                      L+sL+ LdL +N+L+ ++P   g
```

FIGURE 11 cont.

```
       15088    421    LHSLVKLDLTDNQLT-TLPL-AGL    442

LRR_typ_2: domain 14 of 14, from 421 to 444: score 21.6, E = 0.018
                *->LpnLreLdLsnNqLtsLPpgaFqg<-*
                   L++L +LdL +NqLt+LP    ++g
       15088    421    LHSLVKLDLTDNQLTTLPLAGLGG    444

//
```

FIGURE 11 cont.

GAP of: FrGcgManager_101_HTAUB3ha_ check: 2817 from: 1 to: 3637

 mLGR6 - 1 (analysis only) - Import - complete

 to: FrGcgManager_101_ITA0fLsO_ check: 3059 from: 1 to: 2711

 corrected human LGR6 (analysis o - Import - complete

 Symbol comparison table:
 /ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/nwsgapdna.cmp
 CompCheck: 8760

          Gap Weight: 12   Average Match: 10.000
       Length Weight: 4   Average Mismatch: 0.000

           Quality: 21826   Length: 3688
             Ratio: 8.051   Gaps: 20
 Percent Similarity: 84.248   Percent Identity: 84.211

        Match display thresholds for the alignment(s):
                   | = IDENTITY
                   : =   5
                   . =   1

 FrGcgManager_101_HTAUB3ha_ x FrGcgManager_101_ITA0fLsO_

                          .
                          .
                          .   .

     901 CCCACAGCTTCGAGGGGCTGCACAATCTGGAGACACTAGACCTGAACTAT 950   MOUSE
               |||||||||||||||||||||||||||||||||||||| |||
       1 ...............GGGCTGCACAATCTGGAGACACTAGACCTGAATTAT 36   HUMAN

     951 AATGAGCTGCAGGAGTTCCCCCTTGGCTATCCGGACCCTGGGCAGACTGCA 1000
           || ||||||||||||||||| |||| |||||||||||||||||||||
      37 AACAAGCTGCAGGAGTTCCCTGTGGCCATCCGGACCCTGGGCAGACTGCA 86

    1001 AGAATTGGGTTTCCATAACAACAACATCAAGGCTATCCCAGAGAAAGCCT 1050
           ||| |||| ||||||||||||||||||||||||||| |||||||| || ||||
      87 GGAACTGGGGGTTCCATAACAACAACATCAAGGCCATCCCAGAAAAGGCCT 136

    1051 TCATGGGCAACCCTCTCCTGCAGACAATACATTTTTATGACAACCCAATC 1100
           |||||||| ||||||||| || ||||| ||||| |||||||| |||||||||
     137 TCATGGGGAACCCTCTGCTACAGACGATACACTTTTATGATAACCCAATC 186

    1101 CAGTTTGTGGGAAGGTCAGCATTCCAGTACCTGTCTAAACTGCATACGCT 1150
           |||||||||||||| || ||||||||||||||| ||||||| || || ||
     187 CAGTTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAAACTCCACACACT 236

    1151 ATCTTTGAATGGTGCCACTGATATCCAAGAGTTCCCAGACCTCAAAGGCA 1200
           |||| ||||||||||| || ||||| ||||| ||||| |||||||||||
     237 ATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGGCA 286

    1201 CCACTAGCCTGGAGATCCTGACCCTGACCCGTGCGGGCATCAGACTGCTC 1250
           |||| |||||||||||||||||||||||||||||| || |||||| | ||||||
     287 CCACCAGCCTGGAGATCCTGACCCTGACCCGCGCAGGCATCCGGCTGCTC 336

    1251 CCACCGGGGAGTGTGCCAACAGCTGCCTAGGCTCCGAATCCTGGAGCTGTC 1300
           ||| |||| ||||||||||||||||| ||||||||| ||||||| |||||
     337 CCATCGGGGGATGTGCCAACAGCTGCCCAGGCTCCGAGTCCTGGAACTGTC 386

```
1301 TCATAATCAGATCGAGGAGTTACCCAGCCTGCACAGATGTCAGAAGCTGG 1350
     ||| ||||| || |||||| | ||||||||||||||| ||||||||  |||
 387 TCACAATCAAATTGAGGAGCTGCCCAGCCTGCACAGGTGTCAGAAATTGG 436

1351 AGGAAATTGGCCTCCGACATAACAGGATCAAGGAAATTGGTGCAGATACC 1400
     ||||||| ||||||| ||| ||| | ||| ||||||||| || || |||
 437 AGGAAATCGGCCTCCAACACAACCGCATCTGGGAAATTGGAGCTGACACC 486

1401 TTCAGCCAGCTGGGCTCCTTGCAAGCTTTAGACCTGAGTTGGAATGCCAT 1450
     |||||||||||| ||||| ||||||| | || || || ||||| |||||
 487 TTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCAT 536

1451 CCGTGCCATCCACCCTGAGGCTTTCTCAACCCTTCGATCCTTGGTTAAGC 1500
     |||  ||||||||||||||| ||||| |||||| | ||| |||| ||||
 537 CCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCACTCCCTGGTCAAGC 586

1501 TGGACCTGACTGACAACCAGCTGACCACACTGCCCCTGGCTGGGCTGGGA 1550
     |||||||||| ||||||||||||||||||||||||||||||||| || ||
 587 TGGACCTGACAGACAACCAGCTGACCACACTGCCCCTGGCTGGACTTGGG 636

1551 GGCCTGATGCACCTGAAGCTCAAAGGGAACTTGGCCCTGTCTCAGGCCTT 1600
     ||| |||||| |||||||||||||||||||| | || || || ||||||||
 637 GGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCAGGCCTT 686

1601 CTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCCTACGCCT 1650
     ||||||||||||||||||||||||||||||||||||||||||| || ||||
 687 CTCCAAGGACAGTTTCCCAAAACTGAGGATCCTGGAGGTGCCTTATGCCT 736

1651 ACCAGTGCTGTGCCTACGGCATCTGTGCCAGCTTCTTCAAGACCTCTGGG 1700
     ||||||||||| |||| || || ||||||||||||||||||| ||||||||
 737 ACCAGTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGG 786

1701 CAGTGGCAGGCCGAGGACTTTCATCCAGAAGAAGAGGAGGCACCAAAGAG 1750
     |||||| |||| || ||| |||| | || || ||||||| | |||| ||
 787 CAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAG 836

1751 GCCCCTGGGTCTCCTTGCTGGACAAGCTGAGAACCACTATGACCTAGACC 1800
     ||||||||| ||||||||  ||||||| ||||||||||||||||  ||||
 837 GCCCCTGGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGACC 886

1801 TGGATGAGCTCCAGATGGGGACAGAGGACTCAAAGCCAAACCCCAGTGTC 1850
     ||||||||||||||| ||| || |||||||||||||||| ||||||||||
 887 TGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCAGTGTC 936

1851 CAGTGCAGCCCTGTTCCAGGCCCCTTCAAGCCCTGCGAGCACCTCTTTGA 1900
     ||||| ||||| |||||||||||||||||||||| ||| ||||||||||
 937 CAGTGTAGCCCTACTCCAGGCCCCTTCAAGCCCTGTGAGTACCTCTTTGA 986

1901 GAGCTGGGGCATCCGCCTTGCTGTGTGGGCCATCGTGCTGCTCTCCGTAC 1950
     ||||||||||||||||||| || ||||||||||||||| ||||||||| |
 987 AAGCTGGGGCATCCGCCTGGCCGTGTGGGCCATCGTGTTGCTCTCCGTGC 1036

1951 TCTGTAACGGGCTGGTGCTGCTGACAGTCTTTGCCAGCGGACCCAGCCCG 2000
     |||| || || ||||||||||||| || || || |||| ||    |||
1037 TCTGCAATGGACTGGTGCTGCTGACCGTGTTCGCTGGCGGGCCTGCCCCC 1086

2001 CTGTCCCCCGTCAAGCTTGTGGTGGGTGCGATGGCAGGCGCCAACGCCCT 2050
     ||| |||| ||||||| |||||||| |||||||||| ||||||||| || |
1087 CTGCCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGGCGCCAACACCTT 1136
```

FIGURE 12

CONT.

```
2051 GACGGGCATTTCCTGTGGTCTCCTGGCCTCTGTGGACGCCTTGACCTATG 2100
     |||  |||||||||||||| ||  || ||||| ||  ||  ||| ||||||  ||
1137 GACTGGCATTTCCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTTTG 1186

2101 GTCAGTTCGCTGAGTATGGAGCCCGCTGGGAGAGCGGTCTGGGCTGCCAG 2150
     |||||||| |||||||| |||||||||||||||||  ||  || |||||||| |
1187 GTCAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGG 1236

2151 GCTACGGGCTTCCTGGCTGTCCTGGGTTCAGAGGCGTCGGTGCTGCTGCT 2200
     || || ||||||||||| ||  || || || ||||| |||||||||||||||
1237 GCCACTGGCTTCCTGGCAGTACTTGGGTCGGAGGCATCGGTGCTGCTGCT 1286

2201 CACACTGGCGGCCGTGCAGTGCAGCATCTCTGTGACCTGCGTCCGAGCCT 2250
     ||| |||||  || ||||||||||||||| |||| ||   |||| ||||| ||||
1287 CACTCTGGCCGCAGTGCAGTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCT 1336

2251 ACGGGAAGGCGCCGTCGCCTGGCAGCGTCCGCGCAGGCGCACTGGGATGC 2300
     | ||||||| | || || |   |||||||| || |||||| |   || || |||
1337 ATGGGAAGTCCCCCTCCCTGGGCAGCGTTCGAGCAGGGGTCCTAGGCTGC 1386

2301 *CTGGCGCTGGCCGGGCTGGCCGCAGCACTGCCGCTGGCCTCGGTGGGAGA 2350
     ||||| ||||| ||||||||||| ||||||||| ||||||||| ||||||||
1387 CTGGCACTGGCAGGGCTGGCCGCCGCACTGCCCCTGGCCTCAGTGGGAGA 1436

2351 GTATGGCGCCTCCCCACTCTGCCTGCCCTACGCCCCACCCGAGGGCCGGC 2400
      || ||  ||||||||||||||||||||||||||||| ||||| ||||| | ||
1437 ATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGCCACCTGAGGGTCAGC 1486

2401 CGGCCGCCCTGGGCTTCGCTGTAGCCCTGGTGATGATGAACTCGCTCTGC 2450
     | || ||||||||||||| | || ||||||||||||||||||||  ||||
1487 CAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACTCCTTCTGT 1536

2451 TTCCTGGTGGTGGCCGGCGCCTACATCAAGCTCTACTGTGACCTGCCACG 2500
     ||||||||| ||||||||| ||||||||||| || |||||||||||||| ||
1537 TTCCTGGTCGTGGCCGGTGCCTACATCAAACTGTACTGTGACCTGCCGCG 1586

2501 GGGTGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGCGCCACGTGGCCT 2550
     ||| |||||||||||||||||||||||||||||||||||| | |||||||||||
1587 GGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCACGTGGCCT 1636

2551 GGCTCATCTTTGCAGATGGCCTCCTCTACTGCCCCGTGGCCTTCCTCAGC 2600
     ||||||||||| ||||| || |||||||||| ||||||||||||||||||
1637 GGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCTCAGC 1686

2601 TTTGCCTCCATGCTGGGCCTCTTCCCTGTCACCCCCGAGGCTGTCAAGTC 2650
     || ||||||||||||||||||||||||||||| ||  |||||| |||||||
1687 TTCGCCTCCATGCTGGGCCTCTTCCCTGTCACGCCCGAGGCCGTCAAGTC 1736

2651 AGTCCTTCTGGTGGTGCTGCCTCTGCCTGCCTGCCTCAACCCACTGCTCT 2700
      ||||| ||||||||||||||  |||||||||||||||||||||||||| |
1737 TGTCCTGCTGGTGGTGCTGCCCCTGCCTGCCTGCCTCAACCCACTGCTGT 1786

2701 ACCTGCTCTTCAACCCTCACTTCCGGGATGACCTTCGGCGGCTCTGGCCA 2750
     |||||||||||||||||  |||||||||||||||||||||||| ||||
1787 ACCTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCC 1836

2751 AGCCCTCGGTCCCCAGGGCCCCTAGCCTACGCTGCAGCCGGTGAGCTGGA 2800
     || |  || |  | ||||||||||||||||| ||||| ||||| ||||||||
1837 CGCGCAGGGGACTCAGGGCCCCTAGCCTATGCTGCGGCCGGGGAGCTGGA 1886
```

FIGURE 12
CONT.

```
2801 GAAGAGCTCCTGCGACTCCACCCAAGCGCTGGTGGCTTTCTCAGATGTGG 2850
     ||||||||||||| || || ||||||| || |||||| || |||||| |||||||
1887 GAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGG 1936

2851 ATCTTATTCTGGAAGCTTCTGAGGCTGGGCAGCCTCCTGGGCTAGAGACC 2900
     |||| |||||||||||||||||||||| |||||||| ||| ||||||||| |||||||
1937 ATCTCATTCTGGAAGCTTCTGAAGCTGGGCGGCCCCCTGGGCTGGAGACC 1986

2901 TATGGCTTCCCTTCAGTGACCCTCATCTCCCGACATCAGCCGGGGGCCAC 2950
     |||||||||||| |||||||||||||||||||||| | || ||||| |||||| |
1987 TATGGCTTCCCCTCAGTGACCCTCATCTCCTGTCAGCAGCCAGGGGCCCC 2036

2951 CAGGCTGGAGGGAAACCATTTTATAGAGTCTGATGGAACCAAGTTTGGGA 3000
     ||||||||||||| | |||||| | |||||| | || || | | | ||||||||
2037 CAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGA 2086

3001 ACCCACAACCTCCCATGAAGGGAGAACTGCTGCTGAAGGCAGAGGGAGCC 3050
     |||| ||||| ||||| | |||||||||||||||||| |||||||||| |
2087 ACCCCCAACCCTCCATGGATGGAGAACTGCTGCTGAGGGCAGAGGGATCT 2136

3051 ACTTTGGCAGGCTGTGGCTCTTCCGTGGGTGGAGCCCTCTGGCCCTCTGG 3100
     || ||||| | |||| || | ||||||| | | | |||||||||
2137 ACGCCAGCAGGTGGAGGCTTGTCAGGGGGTGGCGGCTTTCAGCCCTCTGG 2186

3101 CTCTCTCTTTGCCTCTCACTTGTAAATATCCCT................. 3133
     ||    ||||||| || ||| |||||||||||||||
2187 CTTGGCCTTTGCTTCACACGTGTAAATATCCCTCCCCATTCTTCTCTTCC 2236

3134 .CTCTGTT...TGTC..CTCTCCCCATC...CAATGATGGCTGCTTATAA 3174
      |||| ||   | || |||||||| ||    ||||||||||||||| |||
2237 CCTCTCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAA 2286

3175 AAGAAAGACAACTCCAAC............TCCATAGCAAGATGGCCAAC 3212
     || ||| |||||   |||           || |||||| ||||||| |
2287 AACAAATACAACCAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCAG 2336

3213 ACCTCTGACTCCATTGTT...CTCTCTCCACGACCCCTAACCAATGAGTG 3259
      | ||| |||||| || |   ||||||||| || | |||||| | |||
2337 TAC.CTGGCTCCACTGATCACCTCTCTCCTGTGACCATCACCAACGGGTG 2385

3260 CTTCCAAGTCTTGCTTTGTCTTGGCCT...TCAGCTTCACTTTCACCCTG 3306
     | ||    | || ||||| ||||||||   ||||||||| || | |||
2386 CCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCTTGATACTG 2435

3307 GGC..CTTCTCTGTCCAATCCAATACTTCTGA.CAGAGGCCTGGGAAATT 3353
     |||  |||| |||| || | || || ||||| ||||| ||
2436 GGCCTCTTCCTTGTCATGTCTGAAGCTGTGGACCAGAGACCTGGACTTTT 2485

3354 ...TGCATAGGAGAAAGGAGAAAAGCAAAAGACAGTGAAGGTTATTGGGC 3400
        ||| || | |||| ||| ||| ||||||||||||||     |||
2486 GTCTGCTTAAGGGAAATGAGGGAAG.TAAAGACAGTGAAG......GGG. 2527

3401 CCTGACAGAGCCATGATCAGTAAGTGCAGAGT.GATGGGGAGGTCTCACA 3449
     ||  |||    |||||    || ||| ||| || |||||  ||||||
2528 ..TG...GAGGGTTGATC....AGGGCACAGTGGACAGGGAGACCTCACA 2568

3450 GAGCATGACACTGGAAGACAACTACCAAAGACATTGGAGAGTCTCCCCTG 3499
     ||| | | | |||||||| | | ||          | | | |||
2569 GAGAAAGGC.CTGGAAGGTGATTTCC.........CGTGTGACTC..... 2603
```

FIGURE 12

CONT.

```
3500  TGACATATAGAATATAAAATGTGTTCTGCGTTCCATTAATCTTGACCTAT 3549
            |    |||| ||| |||||||||||     || ||||||||||||||| |||
2604  ..ATGGATAGGATACAAAATGTGTTCCATGTACCATTAATCTTGACATAT 2651

3550  GCTGNGCCAAAGTGCTTCCTGTTAAAATACACTTTGGAAGACATTGAAAA 3599
            || :|| || |||||| ||||||| ||||||||||| ||| ||||
2652  GCCATGCATAAAGACTTCCTATTAAAATAAGCTTTGGAAGAGATTAAAAA 2701

3600  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 3637
            ||||||||||
2702  AAAAAAAAA............................... 2711
```

FIGURE 12

CONT.

```
GAP of: FrGcgManager_102_MTA0uXMaE  check: 8470  from: 1  to: 968

mLGR6.aa (analysis only) - Import - complete

to: FrGcgManager_102_NTAf7nCl_  check: 5092  from: 1  to: 737

corrected hLGR6.aa (analysis onl - Import - complete

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62
CompCheck: 1102
 Matrix made by matblas from blosum62.iij

        Gap Weight:       12     Average Match:   2.778
     Length Weight:        4     Average Mismatch: -2.248

          Quality:   3424              Length:    968
            Ratio:   4.646                Gaps:      0
Percent Similarity: 90.773     Percent Identity: 89.281

       Match display thresholds for the alignment(s):
                  | = IDENTITY
                  : =   2
                  . =   1


FrGcgManager_102_MTA0uXMaE x FrGcgManager_102_NTAf7nCl_


                  .              .         .            .
    201 IPDYAFQNLTSLVVLHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEFP 250   MOUSE
                                          ||||||||||||||.|||||
      1 ...............................GLHNLETLDLNYNKLQEFP 19    HUMAN

    251 LAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 300
         .|||||||||||||||||||||||||||||||||||||||||||||||||
     20 VAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 69

    301 FQYLSKLHTLSLNGATDIQEFPDLKGTTSLEILTLTRAGIRLLPPGVCQQ 350
         ||||  |||||||||| |||||||||||||||||||||||||||| |.|||
     70 FQYLPKLHTLSLNGAMDIQEFPDLKGTTSLEILTLTRAGIRLLPSGMCQQ 119

    351 LPRLRILELSHNQIEELPSLHRCQKLEEIGLRHNRIKEIGADTFSQLGSL 400
         |||||:|||||||||||||||||||||||||||.|||| |||||||||| ||
    120 LPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSL 169

    401 QALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLMHLKL 450
         |||||||||||.||||||||| |||||||||||||||||||||||||||||
    170 QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKL 219

    451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFFKTSGQWQAEDF 500
         |||||||||||||||||||||||||||||| ||.|||||| ||||:|||
    220 KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDL 269

    501 HPEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSPVPG 550
         | ::||. ||||||||| ||||||| ||||||:  |||||.|||||||| ||
    270 HLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPG 319

    551 PFKPCEHLFESWGIRLAVWAIVLLSVLCNGLVLLTVFASGPSPLSPVKLV 600
         ||||||:||||||||||||||||||||||||||||||||| ||.|| ||| |
    320 PFKPCEYLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFV 369
```

FIGURE 13

```
601 VGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGLGCQATGFLAV 650
    |||.|||| ||||||||||||||||:|||.||||||||.||||.||||||||
370 VGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAV 419

651 LGSEASVLLLTLAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLA 700
    |||||||||||||||||||:||.|||||||.|| |||||| |||||||||
420 LGSEASVLLLTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLA 469

701 AALPLASVGEYGASPLCLPYAPPEGRPAALGFAVALVMMNSLCFLVVAGA 750
    |||||||||||||||||||||||||.|||||| ||||||||| |||||||
470 AALPLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMMNSFCFLVVAGA 519

751 YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL 800
    ||||||||||||||||||||||||||||||||||||||||||||||||||
520 YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL 569

801 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLWPSPRSPGP 850
    ||||||||||||||||||||||||||||||||||||||||||||| |  ||
570 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLRPRAGDSGP 619

851 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGQPPGLETYGFPSVT 900
    ||||||||||||||||||||||[||||||||||||||||.||||||||||||
620 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFPSVT 669

901 LISRHQPGATRLEGNHFIESDGTKFGNPQPPMKGELLLKAEGATLAGCGS 950
    |||  |||| ||||.| :| :|  |||||| | |||||:|||.| || |
670 LISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGL 719

951 SVGGALWPSGSLFASHL* 968
    |  ||    |||  ||||.|
720 SGGGGFQPSGLAFASHV* 737
```

FIGURE 13
CONT.

>15088
> Fbh150881 - Import - vector trimmed
CCGCCSGCGGTGCAGCCCGCCGGGGACCGGGAGGCGGCAGCTGCGGCCACCGCGCCGTGCG
TCCGCGCCCGGCCGCCAGGTGCCCCAGTAGCCCGACCGCCGAGATGCCCAGCCCGCCGGG
GCTCCGGGCGCTATGGCTTTGCGCCGCGCTGTGCGCTTCCCGGAGGGCCGGCGGCGCCCC
CCAGCCCGGCCCGGGGCCCACCGCCTGCCCGGCCCCCTGCCACTGCCAGGAGGACGGCAT
CATGCTGTCTGCCGACTGCTCTGAGCTCGGGCTGTCCGCCGTTCCGGGGGACCTGGACCC
CCTGACGGCTTACCTGGACCTCAGCATGAACAACCTCACAGAGCTTCAGCCTGGCCTCTT
CCACCACCTGCGCTTCTTGGAGGAGCTGCGTCTCTCTGGGAACCATCTCTCACACATCCC
AGGACAAGCATTCTCTGGTCTCTACAGCCTGAAAATCCTGATGCTGCAGAACAATCAGCT
GGGAGGAATCCCCGCAGAGGCGCTGTGGGAGCTGCCGAGCCTGCAGTCGCTGCGCCTAGA
TGCCAACCTCATCTCCCTGGTCCCGGAGAGGAGCTTTGAGGGGCTGTCCTCCCTCCGCCA
CCTCTGGCTGGACGACAATGCACTCACGGAGATCCCTGTCAGGGCCCTCAACAACCTCCC
TGCCCTGCAGGCCATGACCCTGGCCCTCAACCGCATCAGCCACATCCCCGACTACGCGTT
CCAGAATCTCACCAGCCTTGTGGTGCTGCATTTGCATAACAACCGCATCCAGCATCTGGG
GACCCACAGCTTCGAGGGGGCTGCACAATCTGGAGACACTAGACCTGAATTATAACAAGCT
GCAGGAGTTCCCTGTGGCCATCCGGACCCTGGGCAGACTGCAGGAACTGGGGTTCCATAA
CAACAACATCAAGGCCATCCCAGAAAAGGCCTTCATGGGGAACCCTCTGCTACAGACGAT
ACACTTTTATGATAACCCAATCCAGTTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAA
ACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGG
CACCACCAGCCTGGAGATCCTGACCCTGACCCGCGCAGGCATCCGGCTGCTCCCATCGGG
GATGTGCCAACAGCTGCCCAGGCTCCGAGTCCTGGAACTGTCTCACAATCAAATTGAGGA
GCTGCCCAGCCTGCACAGGTGTCAGAAATTGGAGGAAATCGGCCTCCAACACAACCGCAT
CTGGGAAATTGGAGCTGACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAG
CTGGAACGCCATCCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCACTCCCTGGTCAA
GCTGGACCTGACAGACAACCAGCTGACCACACTGCCCCTGGCTGGACTTGGGGGCTTGAT
GCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCCAGGCCTTCTCCAAGGACAGTTTCCC
AAAACTGAGGATCCTGGAGGTGCCTTATGCCTACCAGTGCTGTCCCTATGGGATGTGTGC
CAGCTTCTTCAAGGCCTCTGGGCAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGA
GTCTTCAAAAAGGCCCCTGGGCCTCCTTGCCAGACAAGCAGAGAACCACTATGACCAGGA
CCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCAGTGTCCAGTGTAG
CCCTACTCCAGGCCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCT
GGCCGTGTGGGCCATCGTGTTGCTCTCCGTGCTCTGCAATGGACTGGTGCTGCTGACCGT
GTTCGCTGGCGGGCCTGCCCCCCTGCCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGG
CGCCAACACCTTGACTGGCATTTCCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTT
TGGTCAGTTCTCTGAGTACGGAGCCCCGCTGGGAGACGGGGCTAGGCTGCCGGGCCCACTGG
CTTCCTGGCAGTACTTGGGTCGGAGGCATCGGTGCTGCTGCTCACTCTGGCCGCAGTGCA
GTGCAGCGTCTCCGTCTCCTGTGTCCGGGCCTATGGGAAGTCCCCCTCCCTGGGCAGCGT
TCGAGCAGGGGTCCTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCCGCACTGCCCCTGGC
CTCAGTGGGAGAATACGGGGGCCTCCCCACTCTGCCTGCCCTACGCGCCACCTGAGGGTCA
GCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGATGAACTCCTTCTGTTTCCTGGT
CGTGGCCGGTGCCTACATCAAACTGTACTGTGACCTGCCGCGGGGCGACTTTGAGGCCGT
GTGGGACTGCGCCATGGTGAGGCACGTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTA
CTGTCCCGTGGCCTTCCTCAGCTTCGCCTCCATGCTGGGCCTCTTCCCTGTCACGCCCGA
GGCCGTCAAGTCTGTCCTGCTGGTGGTGCTGCCCCTGCCTGCCTGCCTCAACCCACTGCT
GTACCTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCCGCGCAGG
GGACTCAGGGCCCCTAGCCTATGCTGCGGCCGGGGAGCTGGAGAAGAGCTCCTGTGATTC
TACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTCTGGAAGCTTCTGAAGCTGG
GCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTCAGTGACCCTCATCTCCTGTCAGCA
GCCAGGGGCCCCCAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGG
GAACCCCCAACCCTCCATGGATGGAGAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGC
AGGTGGAGGCTTGTCAGGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTCACA
CGTGTAAATATCCCTCCCCATTCTTCTCTTCCCCTCTCTTCCCTTTCCTCTCTCCCCCTC
GGTGAATGATGGCTGCTTCTAAAACAAATACAACCAAAACTCAGCAGTGTGATCTATAGC
AGGATGGCCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGACCATCACCAACGGGT
GCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCTTGATACTGGGCCTCTTC
CTTGTCATGTCTGAAGCTGTGGACCARAGACCTGGACTTTTGTCTGCTTAAGGGAAATGA
GGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCT
CACARAAAAAGGCCTGGAAGGKGATTTCCCGTGTGACTCATGGRTAGGAWACAAAATGTG
TTCCATGTACCATTAATCTTGACATATGCCATGCATAAARACTTCCTATTAAAATAAGCT
TTGGRAGAGATT

>15088
MPSPPGLRALWLCAALCASRRAGGAPQPGPGPTACPAPCHCQEDGIMLSADCSELGLSAVPGDLDPLTAYLDLSMNNLT
ELQPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS
SLRHLWLDDNALTEIPVRALNNLPALQAMTLALNRISHIPDYAFQNLTSLVVLHLHNNRIQHLGTHSFEGLHNLETLDLNYNK
LQEFPVAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSAFQYLPKLHTLSLNGAMDIQEFPDLKGTT
SLEILTLTRAGIRLLPSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSLQALDLSWNAIR
SIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKLKGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASG
QWEAEDLHLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPCEYLFESWGIRLAVWAIVL
LSVLCNGLVLLTVFAGGPAPLPPVKFVVGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAVLGSE
ASVLLLTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLAAALPLASVGEYGASPLCLPYAPPEGQPAALGFTVA
LVMMNSFCFLVVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGLFPVTPEAVKSVLLVVL
PLPACLNPLLYLLFNPHFRDDLRRLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFP
SVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGLSGGGGFQPSGLAFASHV*

FIGURE 15

protein alignment between mouse and human
> LGR6.

15088m(analysis only) - Import - complete

to: FrGcgManager_9_QBAsD4iW_   check: 8637   from: 1 to: 968

15088h(analysis only) - Import - complete

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62
CompCheck: 1102
 Matrix made by matblas from blosum62.iij

           Gap Weight: 12   Average Match: 2.778
        Length Weight: 4   Average Mismatch: -2.248

              Quality: 4495   Length: 968
                Ratio: 4.653   Gaps: 2
   Percent Similarity: 91.097   Percent Identity: 89.855

          Match display thresholds for the alignment(s):
                      | = IDENTITY
                      : =   2
                      . =   1

FrGcgManager_9_PBA0KgkFJ x FrGcgManager_9_QBAsD4iW_ March 15, 19101 15:24

       1 MHSPPGLLALWLCAVLCASARGGSDPQPGPGRPACPAPCHCQEDGIMLSA 50 Mouse
         | ||||| |||||| |||| | | |||||| |||||||||||||||||||
       1 MPSPPGLRALWLCAALCASRRAGGAPQPGPGPTACPAPCHCQEDGIMLSA 50 Human

      51 DCSELGLSVVPADLDPLTAYLDLSMNNLTELQPGLFHHLRFLEELRLSGN 100
         ||||||||| || |||||||||||||||||||||||||||||||||||||
      51 DCSELGLSAVPGDLDPLTAYLDLSMNNLTELQPGLFHHLRFLEELRLSGN 100

     101 HLSHIPGQAFSGLHSLKILMLQSNQLRGIPAEALWELPSLQSLRLDANLI 150
         |||||||||||||:|||||||.||| |||||||||||||||||||||||
     101 HLSHIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSLRLDANLI 150

     151 SLVPERSFEGLSSLRHLWLDDNALTEIPVRALNNLPALQAMTLALNHIRH 200
         |||||||||||||||||||||||||||||||||||||||||||| | |
     151 SLVPERSFEGLSSLRHLWLDDNALTEIPVRALNNLPALQAMTLALNRISH 200

     201 IPDYAFQNLTSLVVLHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEFP 250
         ||||||||||||||||||||||||||.|||.|||||||| ||||||.|||||
     201 IPDYAFQNLTSLVVLHLHNNRIQHLGTHNFEGLHNLEPLDLNYNKLQEFP 250

     251 LAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 300
         .|||||||||||||||||||||||||||||||||||||||||||||||||
     251 VAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 300

     301 FQYLSKLHTLSLNGATDIQEFPDLKGTTSLEILTLTRAGIRLLPPGVCQQ 350
         |||| ||||||||| |||||||||||||||||||||||||||| |.|||
     301 FQYLPKLHTLSLNGAMDIQEFPDLKGTTSLEILTLTRAGIRLLPSGMCQQ 350

FIGURE 16

```
351 LPRLRILELSHNQIEELPSLHRCQKLEEIGLRHNRIKEIGADTFSQLGSL 400
    |||||:||||||||||||||||||||||||||.||||  ||||||||| ||
351 LPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSL 400

401 QALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLMHLKL 450
    |||||||||||.|||||||||  |||||||||||||||||||||||||||
401 QALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKL 450

451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFFKTSGQWQAEDF 500
    ||||||||||||||||||||||||||||||  ||.||||||  ||||:|||
451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDL 500

501 HPEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNPSVQCSPVPG 550
    |  ::||.  |||||||| ||||||| ||||||:   |||||.||||||| ||
501 HLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPG 550

551 PFKPCEHLFESWGIRLAVWAIVLLSVLCNG.VLLTVFASGPSPLSP.KLV 598
    ||||||:||||||||||||||||||||||| |||||||  ||.||  |  |  |
551 PFKPCEYLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPPVKFV 600

599 VGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGLGCQATGFLAV 648
    |||.||||  ||||||||||||||||||:|||.||||||||.||||.||||||||
601 VGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAV 650

649 LGSEASVLLLTLAAVQCSISVTCVRAYGKAPSPGSVRAGALGCLALAGLA 698
    ||||||||||||||||||:||.||||||||.|| |||||| ||||||||||
651 LGSEASVLLLTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLA 700

699 AALPLASVGEYGASPLCLPYAPPEGRPAALGFAVALVMMNSLCFLVVAGA 748
    |||||||||||||||||||||||||.|||||| |||||||| ||||||||
701 AALPLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMMNSFCFLVVAGA 750

749 YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL 798
    ||||||||||||||||||||||||||||||||||||||||||||||||||
751 YIKLYCDLPRGDFEAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL 800

799 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLWPSPRSPGP 848
    |||||||||||||||||||||||||||||||||||||||||||| |    ||
801 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRRLRPRAGDSGP 850

849 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGQPPGLETYGFPSVT 898
    |||||||||||||||||||||||||||||||||||.|||||||||||||||
851 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFPSVT 900

899 LISRHQPGATRLEGNHFIESDGTKFGNPQPPMKGELLLKAEGATLAGCGS 948
    |||  ||||  ||||.| :| :|  |||||| |  ||||:|||.| ||  |
901 LISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLLRAEGSTPAGGGL 950

949 SVGGALWPSGSLFASHL* 966
    |  ||   ||| ||||.|
951 SGGGGFQPSGLAFASHV* 968
```

FIGURE 16 cont.